

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:41:41 ; Search time 43.94 seconds
(without alignments)
90.053 Million cell updates/sec

Title: US-09-825-561A-10
Perfect score: 850
Sequence: 1 MRSSPGNMRIVICIMVIFL.....LQKMIHQHLSRTGSEDS 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 segs, 24425594 residues
Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2.6/prodata/2/1aa/5A.COMB.pep: *
2: /cgn2.6/prodata/2/1aa/5B.COMB.pep: *
3: /cgn2.6/prodata/2/1aa/6A.COMB.pep: *
4: /cgn2.6/prodata/2/1aa/6B.COMB.pep: *
5: /cgn2.6/prodata/2/1aa/6C.COMB.pep: *
6: /cgn2.6/prodata/2/1aa/6D.COMB.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	850	100.0	162	4	US-09-522-217-2
2	695.5	81.8	519	4	US-09-522-217-85
3	486	57.2	146	4	US-09-522-217-56
4	394	46.4	510	4	US-09-522-217-89
5	212	20.7	40	4	US-09-522-217-72
6	176	20.7	32	4	US-09-522-217-73
7	99.5	11.7	114	1	US-08-031-399-12
8	99.5	11.7	114	1	US-08-031-399-12
9	99.5	11.7	114	1	US-08-393-305-3
10	99.5	11.7	114	1	US-08-726-817-3
11	99.5	11.7	114	1	US-08-504-042-6
12	99.5	11.7	114	1	US-08-504-042-12
13	99.5	11.7	114	2	US-08-725-969-3
14	99.5	11.7	114	2	US-08-794-524-3
15	99.5	11.7	114	4	US-09-189-193-3
16	99.5	11.7	114	5	PCT-US94-03793-6
17	99.5	11.7	114	5	PCT-US94-03793-12
18	99.5	11.7	162	1	US-08-031-399-5
19	99.5	11.7	162	1	US-08-393-305-2
20	99.5	11.7	162	1	US-08-535-733-2
21	99.5	11.7	162	1	US-08-726-817-2
22	99.5	11.7	162	1	US-08-504-042-5
23	99.5	11.7	162	2	US-08-725-969-2
24	99.5	11.7	162	2	US-08-794-524-2
25	99.5	11.7	162	3	US-08-842-947-6
26	99.5	11.7	162	4	US-09-189-193-2
27	99.5	11.7	162	4	US-09-522-217-113

28	99.5	11.7	162	5	PCT-US94-03793-5	Sequence 5, Appl
29	99.5	11.7	162	1	US-08-06423-2	Sequence 2, Appl
30	94.5	11.1	114	1	US-08-031-399-3	Sequence 3, Appl
31	94.5	11.1	114	1	US-08-393-305-6	Sequence 6, Appl
32	94.5	11.1	114	1	US-08-726-817-6	Sequence 6, Appl
33	94.5	11.1	114	1	US-08-504-042-3	Sequence 3, Appl
34	94.5	11.1	114	2	US-08-725-969-6	Sequence 6, Appl
35	94.5	11.1	114	2	US-08-794-524-6	Sequence 6, Appl
36	94.5	11.1	114	4	US-09-189-193-6	Sequence 6, Appl
37	94.5	11.1	114	5	PCT-US94-03793-3	Sequence 3, Appl
38	94.5	11.1	122	1	US-08-300-903A-3	Sequence 3, Appl
39	94.5	11.1	162	1	US-08-031-399-2	Sequence 2, Appl
40	94.5	11.1	162	1	US-08-393-305-5	Sequence 5, Appl
41	94.5	11.1	162	1	US-08-284-393B-9	Sequence 9, Appl
42	94.5	11.1	162	1	US-08-726-817-5	Sequence 5, Appl
43	94.5	11.1	162	1	US-08-504-042-2	Sequence 2, Appl
44	94.5	11.1	162	2	US-08-725-969-5	Sequence 5, Appl
45	94.5	11.1	162	2	US-08-794-524-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-522-217-2
Sequence 2, Application US/09522217
Patent No. 6307024
GENERAL INFORMATION:
APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA1 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-09-522-217-2

Query Match 100.0% Score 850; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 4.8e-87;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMRIVICIMVIFLGLTVHKSSSGOGDRHMRMQLIDYDQKNTYNDLVPEF 60
DB 1 MRSSPGNMRIVICIMVIFLGLTVHKSSSGOGDRHMRMQLIDYDQKNTYNDLVPEF 60
QY 61 LAPADVEFNCSWAFSCFOKAOLKSANTGNENIIVASTIKKKRPSTNAGRQKHL 120
DB 61 LAPADVEFNCSWAFSCFOKAOLKSANTGNENIIVASTIKKKRPSTNAGRQKHL 120
QY 121 TPCSDSYEKKKPEFLERFKSLQKMIHQHLSRTGSEDS 162
DB 121 TPCSDSYEKKKPEFLERFKSLQKMIHQHLSRTGSEDS 162

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RESULT 2
US-09-522-217-85
; Sequence 85, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; EARLIER FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-human zalpha11 ligand fusion polypeptide
US-09-522-217-85

Query Match      81.8%; Score 695.5; DB 4; Length 519;
Best Local Similarity 95.7%; Pred. No. 3.3e-69;
Matches 134; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 23 LVHKSSGQDRHMTIMROLIDIVDOLKNYVDLPEFLPAPEDVETNCENSAFSCFOKA 82
DB 383 LVRGSG---QDRHMTIMROLIDIVDOLKNYVDLPEFLPAPEDVETNCENSAFSCFOKA 439
QY 83 QLSANTGNERTINVSITKIKRKPSTNAGRROKHRLTSCSCSYEKKKPKFELEFKS 142
DB 440 QLSANTGNERTINVSITKIKRKPSTNAGRROKHRLTSCSCSYEKKKPKFELEFKS 499
143 LQKMIHOLSLSTRGSEDS 162
DB 500 LQKMIHOLSLSTRGSEDS 519

RESULT 3
US-09-522-217-56
; Sequence 56, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
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; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 146
; TYPE: PRT
; ORGANISM: mus musculus
US-09-522-217-56
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Query Match      57.2%; Score 486; DB 4; Length 146;
Best Local Similarity 63.0%; Pred. No. 1.2e-46;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERVICLMTVFLCTLVHKSSGQDRHMTIMROLIDIVDOLKNYVDLPEFLPAPEDV 67
DB 1 MERTVCLVFLCTLVHAKSSPGQDRHMTIMROLIDIVDOLKNYVDLPEFLPAPEDV 60
QY 68 ETNCENSAFSCFOKAQLKSANTGNERTINVSITKIKRKPSTNAGRROKHRLTSCSCS 127
DB 61 KGHCHAAFAFCQAKLKPSPNKNKTFIDVLAQLRRRLPARGGKKQKHIAKCPSCDS 120
QY 128 YEKKPKFELEFKSLQKMIHOLS 153
DB 121 YEKKPKFELEFKSLQKMIHOLS 146
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RESULT 4
US-09-522-217-89
; Sequence 89, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 89
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-mouse zalpha11 ligand fusion polypeptide
US-09-522-217-89
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Query Match      46.4%; Score 394; DB 4; Length 510;
Best Local Similarity 62.0%; Pred. No. 1.1e-35;
Matches 75; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

QY 33 DRHMTIMROLIDIVDOLKNYVDLPEFLPAPEDVETNCENSAFSCFOKAQLKSANTGN 92
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Fri Jun 28 07:58:54 2002

us-09-825-561a-10.raii

Page 4

[illegible]

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      RESULT      8
US-08-031-399-12
      : Sequence 12, Application US/08031399
      : Patent No. 5552303
      :
      : GENERAL INFORMATION:
      :
      : APPLICANT: Grabstein, Kenneth
      :
      : APPLICANT: Anderson, Dirk
      :
      : APPLICANT: Eisenman, June
      :
      : APPLICANT: Fung, Victor
      :
      : APPLICANT: Rauch, Charles
      :
      : TITLE OF INVENTION: Epithelium-derived T-cell Factor
      :
      : NUMBER OF SEQUENCES: 12
      :
      : CORRESPONDENCE ADDRESS:
      :
      : ADDRESSEE: Immunex Corporation
      :
      : STREET: 51 University Street
      :
      : CITY: Seattle
      :
      : STATE: Washington
      :
      : COUNTRY: USA
      :
      : ZIP: 98101
      :
      : COMPUTER READABLE FORM:
      :
      : MEDIUM TYPE: Floppy disk
      :
      : COMPUTER: IBM PC compatible
      :
      : OPERATING SYSTEM: PC-DOS/MS-DOS
      :
      : SOFTWARE: Patentia Release #1.0, Version #1.25
      :
      : CURRENT APPLICATION DATA:
      :
      : APPLICATION NUMBER: US/08/031,399
      :
      : FILING DATE: 19930308
      :
      : CLASSIFICATION: 530
      :
      : ATTORNEY/AGENT INFORMATION:
      :
      : NAME: Launer, Charlene
      :
      : REGISTRATION NUMBER: 33,035
      :
      : REFERENCE/DOCKET NUMBER: 2811
      :
      : TELECOMMUNICATION INFORMATION:
      :
      : TELEPHONE: 206-587-0430
      :
      : INFORMATION FOR SEQ ID NO: 12:
      :
      : SEQUENCE CHARACTERISTICS:
      :
      : LENGTH: 114 amino acids
      :
      : TYPE: AMINO ACID
      :
      : TOPOLOGY: linear
      :
      : MOLECULE TYPE: protein
      :
      : HYPOTHEICAL: NO
US-08-031-399-12

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Query Match 11.7% Score 99.5 DB 1 Length 114:
Best Local Similarity 25.2% Pred. No. 0.00086:
Matches 30; Conservative 23; Mismatches 45; Indels 21; Gaps 5

Qy      43 IDIVDOLKANYNDLYPE-----LPAPEDVETNCESMSHSCF-QKQDLKSANTGNN---- 92
       :::: | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      3 VNIISLKL-IEDLIOSMIDATLYTESYVHSCKCYAMCFLLEIQLTVISSESGPXIH 61

Qy     93 --ERIINYSIKLLRKRPSTNAGROKHRLTSPCSDEYEKKPKFELEFRFKSLQKMII 149
       | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     62 IVENITILLANXXLSNGNXTESS-----CKKEEELERENIKRLEPLQSFVAHYQMFIN 112

RESULT          9
US-08-393-305-3
Sequence 3, Application US/08393305
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? Patent No. 5574138
?
? GENERAL INFORMATION:
? APPLICANT: Grabstein, Kenneth
? APPLICANT: Anderson, Dirk
? APPLICANT: Eisenman, June
? APPLICANT: Fung, Victor
? APPLICANT: Rauch, Charles
? TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
? NUMBER OF SEQUENCES: 15
? CROSS-REFERENCE ADDRESSES:
? ADDRESSEE: Seed and Berry
? STREET: 6300 Columbia Center, 701 Fifth Avenue
? CITY: Seattle
? STATE: Washington
? COUNTRY: USA
? ZIP: 98104
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/393,305
? FILING DATE: 22-FEB-1995
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: Mcmasters, David D.
? REGISTRATION NUMBER: 33,963
? REFERENCE/DOCKET NUMBER: 480052,409C2
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 206-622-4900
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 114 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
?
? MOLECULE TYPE: protein
?
? US-08-393-305-3

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,817
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-726-817-3

Query Match 11.7%; Score 99.5; DB 1; Length 114;
Best Local Similarity 25.9%; Pred. No. 0.00086;
Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;

OY 43 IDIVDLKKNVNDVPER-----LPAPDEVETNCWMSAFSCF-----QKAOLKSANTGNNE 93
DB 3 VNVISDLKK-IEDLIQSMHIDATLYTESDVHPSCVTAMKCFLLLEQVLSLESGDASHD 61
OY 94 RIIVSIRKIKRRPPSTNAGRQRKRLTSPSCDSYERKPPKEFLERFKSLQKMH 149
DB 62 TVENLIT--LANNSLSSNGVNTES---GCKECELEEKNIKKEFLQSFVHIQMFIN 112

RESULT 11
US-08-504-042-6
Sequence 6, Application US/08504042
Patent No. 5747024
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: Epithelium-derived T-cell Factor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504,042
FILING DATE: 19-JUL-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/031,399
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Launer, Charlene
REGISTRATION NUMBER: 33,035

REFERENCE/DOCKET NUMBER: 2811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-504-042-6

Query Match 11.7%; Score 99.5; DB 1; Length 114;
Best Local Similarity 25.9%; Pred. No. 0.00086;
Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;

OY 43 IDIVDLKKNVNDVPER-----LPAPDEVETNCWMSAFSCF-----QKAOLKSANTGNNE 93
DB 3 VNVISDLKK-IEDLIQSMHIDATLYTESDVHPSCVTAMKCFLLLEQVLSLESGDASHD 61
OY 94 RIIVSIRKIKRRPPSTNAGRQRKRLTSPSCDSYERKPPKEFLERFKSLQKMH 149
DB 62 TVENLIT--LANNSLSSNGVNTES---GCKECELEEKNIKKEFLQSFVHIQMFIN 112

RESULT 12
US-08-504-042-12
Sequence 12, Application US/08504042
Patent No. 5747024
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: Epithelium-derived T-cell Factor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504,042
FILING DATE: 19-JUL-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/031,399
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Launer, Charlene
REGISTRATION NUMBER: 33,035
REFERENCE/DOCKET NUMBER: 2811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-504-042-12

RESULT 14

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/189,193
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-189-193-3

Query Match 11.7%; Score 99.5; DB 4; Length 114;
Best Local Similarity 25.9%; Pred. No. 0.00086;
Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;
QY 43 IDIVDQLKNVYNDLVPEF----LPAPDYETNCEWSAFSCF---QKAOLKSANTGNNE 93
DB 3 VNVISDLKK-IEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLELQVTSLESGDASIH 61
QY 94 RIINVSIRKLKRPSTNAGRRQKRLTGPCSDSYEKKKRPKEFLERFKSLQKMIH 149
DB 62 IVENLII--LANNSSISNGNVTES--GCKECELEEKNIKIFLQSFVHIVQMPIN 112

Search completed: June 28, 2002, 07:41:41
Job time: 56 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2002, 07:41:39 ; Search time 43.94 Seconds
(Without alignments)
121.183 Million cell updates/sec

Title: US-09-825-561A-6

Sequence: 1 CPDLVCYDYDQIVICILEM.....SDPVIFQOQSEELKEGMNPH 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 231628 seqs, 24425594 residues

total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: Issued_Patents_AA:*
2: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1195	100.0	538	3	US-09-040-005-2
2	1195	100.0	538	4	US-09-522-217-115
3	1195	100.0	606	4	US-09-522-217-97
4	144	12.1	894	2	US-08-599-455B-2
5	144	12.1	894	4	US-09-069-781B-2
6	144	12.1	894	4	US-08-618-957A-12
7	144	12.1	1162	2	US-08-599-455B-43
8	144	12.1	1162	4	US-09-069-781B-12
9	142.5	11.9	896	2	US-08-640-389A-12
10	141.5	11.8	539	6	5198359-4
11	141.5	11.8	539	6	5449756-4
12	139	11.6	493	2	US-08-078-311-7
13	139	11.6	493	2	US-08-460-402-7
14	139	11.6	635	1	US-08-184-327A-4
15	139	11.6	635	2	US-08-078-311-1
16	139	11.6	635	2	US-08-460-402-1
17	139	11.6	635	5	PCT-US95-00670-4
18	138	11.5	895	4	US-08-827-962-19
19	138	11.5	1162	4	US-08-827-962-15
20	138	11.5	1162	4	US-08-803-346-1
21	137	11.5	1165	2	US-08-589-455B-4
22	137	11.5	1165	4	US-09-093-814-1
23	137	11.5	1165	4	US-09-069-781B-4
24	137	11.5	1165	4	US-08-618-957A-11
25	136	11.4	569	1	US-08-306-231-3
26	136	11.4	896	4	US-08-618-957A-10
27	136	11.4	898	2	US-08-693-697-36

ALIGNMENTS

28	136	11.4	906	4	US-08-618-957A-9	Sequence 9, Appl
29	136	11.4	908	2	US-08-693-697-33	Sequence 33, Appl
30	136	11.4	908	2	US-08-588-526-3	Sequence 3, Appl
31	136	11.4	958	4	US-08-618-957A-8	Sequence 8, Appl
32	136	11.4	960	1	US-08-355-888A-8	Sequence 8, Appl
33	136	11.4	960	2	US-08-588-190-3	Sequence 3, Appl
34	136	11.4	960	2	US-08-693-697-8	Sequence 8, Appl
35	136	11.4	960	2	US-08-618-957A-3	Sequence 3, Appl
36	136	11.4	960	2	US-08-693-697-8	Sequence 8, Appl
37	136	11.4	960	4	US-08-618-957A-3	Sequence 3, Appl
38	135	11.3	1162	4	US-08-827-962-20	Sequence 20, Appl
39	133.5	11.2	369	2	US-08-424-224-2	Sequence 2, Appl
40	133.5	11.2	369	5	PCT-US94-02891-69	Sequence 69, Appl
41	132.5	11.1	382	2	US-08-078-311-3	Sequence 3, Appl
42	132.5	11.1	382	2	US-08-460-402-3	Sequence 3, Appl
43	132.5	11.1	482	1	US-08-184-327A-8	Sequence 8, Appl
44	132.5	11.1	482	5	PCT-US95-00670-8	Sequence 8, Appl
45	132.5	11.1	626	1	US-08-184-327A-2	Sequence 2, Appl

RESULT 1
US-09-040-005-2
; Sequence 2, Application US/09040005
; Patent No. 6057128
; GENERAL INFORMATION:
; APPLICANT: Donaldson, Debra
; APPLICANT: Unger, Michelle
; TITLE OF INVENTION: MU-1 RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,005
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A 32,724
; REGISTRATION NUMBER: G15320
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-498-8224
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 538 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-040-005-2

Query Match 100.0%; Score 1195; DB 3; Length 538;
Best Local Similarity 100.0%; Pred. No. 7.1e-123; Indels 0; Gaps 0;
Matches 218; Conservative 0; Mismatches 0;

QY 1 CPDLVCYDYDQIVICILEMNLHPSTLTLTWQDOYELKDEATSCSLHRSANATHATY 60
DB 20 CPDLVCYDYDQIVICILEMNLHPSTLTLTWQDOYELKDEATSCSLHRSANATHATY 79

Fri Jun 28 07:59:00 2002

us-09-825-561a-6.rai

Page 3

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1 OPERATING SYSTEM: Windows95
2 SOFTWARE: FASTSEQ for Windows Version 2.0
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/08/599,455B
5 FILING DATE: 22-JAN-1996
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: 08/583,153
8 FILING DATE: 28-DEC-1995
9 APPLICATION NUMBER: 08/570,142
10 FILING DATE: 11-DEC-1995
11 APPLICATION NUMBER: 08/569,485
12 FILING DATE: 08-DEC-1995
13 APPLICATION NUMBER: 08/566,622
14 FILING DATE: 04-DEC-1995
15 APPLICATION NUMBER: 08/562,663
16 FILING DATE: 27-NOV-1995
17 ATTORNEY/AGENT INFORMATION:
18 NAME: Melkielejohn, Ph.D., Anita L.
19 REGISTRATION NUMBER: 35,283
20 REFERENCE/DOCKET NUMBER: 07334/017001
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: 617-542-5070
23 TELEFAX: 617-542-8906
24 TELEX: 200154
25 INFORMATION FOR SEQ ID NO: 2:
26 SEQUENCE CHARACTERISTICS:
27 LENGTH: 894 amino acids
28 TYPE: amino acid
29 TOPOLOGY: linear
30 MOLECULE TYPE: protein
31 FRAGMENT TYPE: Internal
32
33 US-08-599-455B-2

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Query Match:                               12.1%: Score 144; DB 2: Length 894;
Best Local Similarity                      31.1%: Pred. No. 4,4e-07;
Matches 57; Conservative 22; Mismatches 60; Indels 44; Gaps 11.

QY      39 LKDE---ATSCGLHRSANATHAITYTCHMDVF-----FMADIFSVNITDQSGNS 87
           ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       177 LKSFQVFOVCNCILRCC-----ECHVPYPRAKLNYALLMYLETTSAGVSOSPPLMS 227
QY      88 QECGSEFLAESIRKAPP--FNVTYFSGGYNSWRSDVEDPAFYMLKGLOVELOYNRC 145
           : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       228 LG--PMLY---VKRPDPPLGIHMEYDDGLKLSMDSQTMAF-----PLQYQKYLENS 276
QY      146 DPMAVSPRRKLIVDSRV-SLLPLEFRKDSYTELVQVACGMPOSSSTQGTWSEKSDPYIF 204
           ::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db       277 T-TVRBAEIVSATSLVDVLP-----GSSEYQVSRSKRLDS---GWSDMSPOVF 326
QY      205 QTQ 207
           ||
Db       327 TTQ 329

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US-09-069-781B-2
: Sequence 2, Application US//09069781B
: Patent No. 6287782
: GENERAL INFORMATION:
    APPLICANT: Tartaglia, Louis A.
    APPLICANT: Tepper, Robert I.
    APPLICANT: Culpepper, Janice A.
    APPLICANT: White, David W.
    TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
    TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
    TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
    NUMBER OF SEQUENCES: 50
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Fish & Richardson, P.C.
    STREET: 225 Franklin Street
    CITY: Boston
    STATE: MA

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1 COUNTRY: US
2 ZIP: 02110-2804
3 COMPUTER READABLE FORM:
4 MEDIUM TYPE: Diskette
5 COMPUTER: IBM Compatible
6 OPERATING SYSTEM: Windows95
7 SOFTWARE: FastSeq for Windows Version 2.0
8
9 CURRENT APPLICATION DATA:
10 APPLICATION NUMBER: US/09/069,781B
11 FILING DATE: 29-APRIL-1998
12
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 08/864,564
15 FILING DATE: 28-MAY-1997
16 APPLICATION NUMBER: US 08/708,123
17 FILING DATE: 03-SEP-1996
18 APPLICATION NUMBER: US 08/638,524
19 FILING DATE: 26-APR-1996
20 APPLICATION NUMBER: US 08/599,455
21 FILING DATE: 22-JAN-1996
22 APPLICATION NUMBER: US 08/583,153
23 FILING DATE: 28-DEC-1995
24 APPLICATION NUMBER: US 08/570,142
25 FILING DATE: 11-DEC-1995
26 APPLICATION NUMBER: US 08/569,485
27 FILING DATE: 08-DEC-1995
28 APPLICATION NUMBER: US 08/566,622
29 FILING DATE: 04-DEC-1995
30 APPLICATION NUMBER: US 08/562,663
31 FILING DATE: 27-NOV-1995
32
33 ATTORNEY/AGENT INFORMATION:
34 NAME: Melkielehn, Ph.D., Anita L.
35 REGISTRATION NUMBER: 35,283
36 REFERENCE/DOCKET NUMBER: 07334/082001
37
38 TELECOMMUNICATION INFORMATION:
39 TELEPHONE: (617) 542-5070
40 TELEFAX: (617) 542-8906
41
42 TELEX: 200154
43
44 INFORMATION FOR SEQ ID NO: 2:
45 SEQUENCE CHARACTERISTICS:
46 LENGTH: 894 amino acids
47 type: amino acid
48 TOPOLOGY: unknown
49
50 MOLECULE TYPE: protein
51 FRAGMENT TYPE: Internal
52
53 US-09-069-781B-2

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Query Match      12.1% ; Score 144 ; Ds 4 ; Length 894 ;
Best Local Similarity 31.1% ; Pred. No. 4,4e-07 ;
Matches 57 ; Conservative 22 ; Mismatches 60 ; Indels 44 ; Gaps 11 ;

QY      39 LKDE---ATSCSLRHSANMATHAITYTCHMDVF-----FMADIFFSVNITDGSNTS 87
           |||      |||      |||      |||      |||      |||      |||      |||
Db      177 LKSFQTVQVCNCSLRSC-----ECHVPPYPRAKLNYALLMLLETTSAGVSFOSPIMS 227

QY      88 QECSSEFLIASIPAP--FNVTYTFESGQYNISWRSDYEDPAFPMLGKGLQYELQYRNG 145
           |||      |||      |||      |||      |||      |||      |||      |||
Db      228 LQ--PMILV---VAPDPPLGLHHEVTDDGNLKTISMDSQTMADF-----PLQYQKLEMS 276

QY      146 DPMANVSRRKLISVDSRSV-SLLPLEFRKDSYELQYNAGMPGSSSYQGTWASEMSDPVTF 204
           |||      |||      |||      |||      |||      |||      |||      |||
Db      277 T--IVRAEALIVSATSLIVDSYLP-----GSSYEYQVSRKRLDSS--GWSMDSSPOVF 326

QY      205 QTQ 207
           ||
Db      327 TTQ 329

RESULT      6
US-08-618-957A-12
; Sequence 12, Application US/08618957A
; Patent No. 6335237
; GENERAL INFORMATION:

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Query Match	12.1%;	Score 144;	DB 4;	Length 894;
Best Local Similarity	31.1%;	Pred. No. 4.4e-07;		
Matches 57;	Conservative 22;	Mismatches 60;	Indels 44;	Gaps 11

RESULT 7
US-08-599-455B-43
; Sequence 43, Application US/08599455B
; Patent No. 5972621
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.

Query Match	12.1%;	Score 144;	DB 2;	Length 1162;
Best Local Similarity	31.1%;	Pred. No. 6.5e-07;		
Matches	57;	Conservative	22;	Mismatches 60;
			Indels	44;
			Gaps	11

RESULT 8
US-09-069-781B-43
; Sequence 43, Application US/09069781B
; Patent No. 6287782


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Db      330  IMENEEEKKNPGIQPFQSRCHFKNRSDSIHIL-----VEVTAPCTVSHSLGSPF 383
Oy      94  LLAESIK-PAPPENVTYTFSGQYIISMRSDYEDPAFYMLGKLOLEYQYNNRG-DPAWVS 151
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     384  WIHOAVRLPTLNLHMREISGHELEW---QHSSWAAQ-ETCYQYLRATYGBECHOIMKV- 437
Oy     152  PRKRIIVDSRSVSLP-----LEFRKDSYELOVRAGPMPGSSYQGTWSEWSDPVI 203
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     438  -----LEPPLGARGGTLELRPSRSYRIQLRA-RLNGPTYYQGPSSWSDSPTR 482
Oy     204  FQFQSE 209
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Db     483  VETATE 488

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RESULT 15
US-08-078-311-1
; Sequence 1, Application US/08078311
; Patent No. 5035750

GENERAL INFORMATION:

APPLICANT: Gisselbrecht, Silvie

APPLICANT: Souyri, Michele

APPLICANT: Varlet, Paul

APPLICANT: Vigon, Isabelle
APPLICANT: Wendling, Francois

TITLE OF INVENTION: Polypeptide

TITLE OF INVENTION: myeloproliferative Disease

CORRESPONDENCE ADDRESS:

ADDRESS: MEICHANUC & GOUNU
STREET: 3100 No. 5925750west Center

CITY: Minneapolis
STATE: MN

COUNTRY: USA

COMPUTER REAI

COMPUTER: IBM PC com

OPERATING SYSTEM: PC-DOS
SOFTWARE: Patent In Rejection

CURRENT APPLICATION DATA:

FILING DATE: 18-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/FR90/00062
 FILING DATE: 19-OCT-1990

ATTORNEY/AGENT INFORMATION:
NAME: Ronald J. Burk
KSTB-01

REGISTRATION NUMBER: 36,848

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-332-3333
TELEFAX: 612-332-9081

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 635 amino acids

TOPOLOGY: linear

MOECODE LIFE. PERCINAE
-08-078-311-1

Query Match	Score	DB 2	Length
11.68	139	2	635

Matches	59;	Conservative	25;	Mismatches	76;	Indels	86;	Gaps	14;
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4 LVCYTDYLOTVICILEMWNLPSTLLTWODOYEELKDEATSCSL--HRSAHNATHATY- 6C

Db	289	LOCFTLDLKNVYC-----QMOOO-----DHASSGPFYHSRACCPDRXP	329
Qy	61	-----TCH-----DYFHADDFSVNITDQSGNLSQEGCS-F	93
Db	330	IWENCEEEKITNGLOTPQFSRCHKSKSNDSITHIL-----VEYITAGVYHSTLGSF	383
Qy	94	LLAEAK-PAPFENVTVTFSGQYNISWRSDEDPAFYMLKGLQYELQYLRNGK-DPMAVS	151
Db	384	WHDGAVRLPTPLMHREITSSGHLEW-----QHSSMAQ-ETCYGLRYTGBGHQDKV-	437
Qy	152	PKRKLLISVDSKSYSLP-----LEPRDSSLELQYVRAGPMPGSSVIGTYSKESDPVI	203
Db	438	-----LEPLGARGGTLELRPSRYRIQLRA-RLNGPTFYQGWGSSWSDPTR	482
Qy	204	FOTQSE	209
Db	483	VEATATE	488

Db 483 VETATE 488

Search completed: June 28, 2002, 07:41:41

000 LINES: 20 SEC

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:43:19 ; search time 20.33 Seconds
(without alignments)
415.192 Million cell updates/sec

Title: US-09-825-561A-6

Perfect score: 1195
Sequence: 1 CPDLVCYTDYLTQTVICILEM.....SDPVIFQTOSEELKEGMNPH 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145	12.1	878	1 IL3B_MOUSE	P26954 mus musculus
2	144	12.1	896	1 CYR2_MOUSE	P26955 mus musculus
3	144	12.1	1162	1 LEPR_MOUSE	P48356 mus musculus
4	141.5	11.8	539	1 IL2B_MOUSE	P16297 mus musculus
5	139	11.6	635	1 TPOR_MOUSE	P40238 mus musculus
6	138	11.5	1162	1 LEPR_MOUSE	P48357 mus musculus
7	137	11.5	1165	1 IL2B_MOUSE	P24994 mus musculus
8	135.5	11.3	825	1 IL2B_MOUSE	P24994 mus musculus
9	134	11.2	537	1 IL2B_MOUSE	P24994 mus musculus
10	133.5	11.2	369	1 CYR2_MOUSE	P34902 mus musculus
11	132.5	11.1	625	1 TPOR_MOUSE	P40238 mus musculus
12	127.5	10.7	379	1 CYR2_MOUSE	P40238 mus musculus
13	127	10.6	373	1 CYR2_MOUSE	P40238 mus musculus
14	126	10.5	551	1 IL2B_MOUSE	P14784 mus musculus
15	123	10.3	459	1 IL2B_MOUSE	P14784 mus musculus
16	122	10.2	831	1 IL2B_MOUSE	P14784 mus musculus
17	122	10.2	918	1 IL2B_MOUSE	P14784 mus musculus
18	120	10.0	369	1 CYR2_MOUSE	P34902 mus musculus
19	118	9.9	862	1 IL2B_MOUSE	P14784 mus musculus
20	118	9.9	862	1 IL2B_MOUSE	P14784 mus musculus
21	117	9.8	810	1 IL2B_MOUSE	P14784 mus musculus
22	115.5	9.7	831	1 IL2B_MOUSE	P14784 mus musculus
23	115	9.6	459	1 IL2B_MOUSE	P14784 mus musculus
24	112.5	9.4	917	1 IL2B_MOUSE	P14784 mus musculus
25	110.5	9.2	918	1 IL2B_MOUSE	P14784 mus musculus
26	108.5	9.1	468	1 IL2B_MOUSE	P14784 mus musculus
27	106	8.9	658	1 IL2B_MOUSE	P14784 mus musculus
28	105.5	8.8	460	1 IL2B_MOUSE	P14784 mus musculus
29	105.5	8.8	460	1 IL2B_MOUSE	P14784 mus musculus
30	105	8.8	522	1 IL2B_MOUSE	P14784 mus musculus
31	104	8.7	522	1 IL2B_MOUSE	P14784 mus musculus
32	103	8.6	508	1 IL2B_MOUSE	P14784 mus musculus
33	102	8.5	468	1 IL2B_MOUSE	P14784 mus musculus

34	99.5	8.3	467	1 IL6A_PIG	O18796 sus scrofa
35	99.5	8.3	507	1 EPOR_MOUSE	P14753 mus musculus
36	99	8.3	420	1 IL5R_HUMAN	O01344 homo sapien
37	97.5	8.2	662	1 IL2R_HUMAN	P42701 homo sapien
38	97	8.1	462	1 IL6A_MOUSE	P22273 rattus norv
39	95	7.9	415	1 IL5R_MOUSE	P21183 mus musculus
40	95	7.9	581	1 PRUR_CEREL	O28235 cervus elap
41	94	7.9	328	1 IL2B_MACMU	P46095 macaca mula
42	94	7.9	611	1 GHR_COLLI	O90375 columba liv
43	93.5	7.8	650	1 GHR_MOUSE	P16882 mus musculus
44	93.5	7.8	874	1 IL2S_MOUSE	P97378 mus musculus
45	93	7.8	327	1 IL2B_CEREL	O28234 cervus elap

ALIGNMENTS

RESULT	1	ALIGNMENTS
IL3B_MOUSE	STANDARD;	PRT; 878 AA.
IL3B_MOUSE		
AC	P26954;	
DT	01-OCT-1993 (Rel. 27, Created)	
DT	01-OCT-1993 (Rel. 27, Last sequence update)	
DT	30-MAY-2000 (Rel. 39, Last annotation update)	
DE	Interleukin-3 receptor class II beta chain precursor (Colony	
DE	stimulating factor 2 receptor, beta 2 chain).	
GN	CSF2RB2 OR A12CA OR IL3RB2 OR IL3R.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_Taxid=10090;	
RM	11	
RP	SEQUENCE FROM N.A.	
RP	MEDLINE=90117145; Pubmed=2404337;	
RA	Itch N., Yonehara S., Schreurs U., Gorman D.M., Maruyama K., Ishii A.,	
RA	Yanara I., Arai K., Miyajima A.;	
RT	"Cloning of an interleukin-3 receptor gene: a member of a distinct	
RT	receptor gene family.";	
RL	Science 247:324-327(1990).	
CC	-1- FUNCTION: IN MOUSE THERE ARE TWO CLASSES OF HIGH-AFFINITY IL-3	
CC	RECEPTORS. ONE CONTAINS THIS IL-3-SPECIFIC BETA CHAIN AND THE	
CC	OTHER CONTAINS THE BETA CHAIN ALSO SHARED BY HIGH-AFFINITY IL-5	
CC	AND GM-CSF RECEPTORS.	
CC	-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.	
CC	-1- SUBCELLULAR LOCATION: TYPE I membrane protein.	
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; M29855; AAA3295.1; -	
DR	PIR; A40091; A40091	
DR	MGD; MGI:1339760; Csf2rb2.	
DR	InterPro; IPR002996; CRIA.	
DR	InterPro; IPR000282; Cytok_receptor_2.	
DR	InterPro; IPR003961; FN_III.	
DR	InterPro; IPR005311; Hematopo_receptor_S_F1.	
DR	SMART; PF00041; fn3; 2.	
DR	SMART; SM00060; FN3; 2.	
DR	PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.	
DR	Receptor; Transmembrane; Glycoprotein; Signal.	
KW	SIGNAL	
FT	CHAIN	1 22
FT	INTERLEUKIN-3 RECEPTOR CLASS II BETA	
FT	CHAIN.	
FT	EXTRACELLULAR (POTENTIAL).	
FT	POTENTIAL.	
FT	TRANSMEM.	441 462
FT	DOMAIN	463 878
FT	CYTOPLASMIC (POTENTIAL).	
FT	BY SIMILARITY.	
FT	DISULFID	39 49

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FT DISULFID 78 95 BY SIMILARITY.
FT DISULFID 254 264 BY SIMILARITY.
FT DISULFID 293 310 BY SIMILARITY.
FT CARBOHYD 350 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 878 AA; 97195 MW; 8EBC9092ADC24D56 CRC64;

Query Match 12.1%; Score 145; DB 1; Length 878;
Best Local Similarity 23.0%; Pred. No. 3.2e-05;
Matches 54; Conservative 30; Mismatches 91; Indels 60; Gaps 9;

QY 4 LVCYDTLQTVICILEMMLHPSTLTWQDQ-----YEEI-KDEATSCSF-- 48
DB 37 LECYNDYTNRIIC-----SWADTEDAQGLIMTLVHOLDKIOSVSCELSE 82
QY 49 -----HRSANAHATATYTCNM-----DYEFHMAODIFSVNITIDSGNSQSCGSEL 94
DB 83 KLMMSECPSSHRCVPRRCVPTPTRESGNDYISFOPDDLCIQL-----MVP 130
95 LAESIKPAPFNTVTFESG-QYNISWRSDYEDPAFYMLKG-LQYELQYRNKGDPAVSP 152
131 LAOHVQPPPKDHIHISPSGDFHLEWVSIGDSQVSMSSKDIIEFEVAYKRLQDSMEDA- 189
QY 153 RRKLISDSSVSLLEPFKQSSYELQYRAGPMGSSYQGTWSEMDSPVIFQTO 207
DB 190 --SLSHTSNQVNDKRLPLPNSITARYRTRLSAGSSLSGRPSRMSPEVHMDSQ 242

RESULT 2
CYRB_MOUSE STANDARD; PRT; 896 AA.
ID CYRB_MOUSE STANDARD; PRT; 896 AA.
AC P26955;
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1993 (Rel. 41, Last annotation update)
DE Cytokine receptor common beta chain precursor.
GN CSF2RB OR CSF2RB1 OR ALC2B OR IL3RB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90319131; PubMed=1695379;
RA Gorman D.M., Itoh N., Kitamura T., Schreurs J., Yonehara S.,
RA Yehara I., Arai K., Miyajima A.;
RT Cloning and expression of a gene encoding an interleukin 3 receptor-
RT like protein: identification of another member of the cytokine
RT receptor gene family";
Proc. Natl. Acad. Sci. U.S.A. 87:5459-5463(1990).
CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5
CC AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M34397; AAA37204.1; -
CC PIR: A35782; A35782.
CC MGI: MGI:1339759; Csf2rb1.
CC Interpro: IPR002996; CR1A.
CC Interpro: IPR000282; Cytok_receptor_2.
CC Interpro: IPR003961; FN_III.

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DR Interpro: IPR003531; Hematopo_receptor_S_F1.
DR Pfam: PF00041; fn3; 2.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 896 CYTOKINE RECEPTOR COMMON BETA CHAIN.
FT DOMAIN 23 441 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 442 463 POTENTIAL.
FT DOMAIN 464 896 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 132 241 FIBRONECTIN TYPE-III 1.
FT DOMAIN 343 440 FIBRONECTIN TYPE-III 2.
FT DISULFID 39 49 BY SIMILARITY.
FT DISULFID 77 92 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 896 AA; 99111 MW; 8CE16DFFC07A999 CRC64;

Query Match 12.1%; Score 144; DB 1; Length 896;
Best Local Similarity 22.6%; Pred. No. 4e-05;
Matches 49; Conservative 41; Mismatches 87; Indels 40; Gaps 9;

QY 3 DLVCYDTLQTVICILEMNN-----LHPSTLTWQDQYEELEKDEATSCSLHRS 51
DB 250 NLQCFDGLDLSGMSWEVNTQTGSYFGLFYRPPVA-----PEKGCSPVYKEP 299
QY 52 AHNAHTATYTCNMDFHFMADIFSVNITIDSGNSQSCGSLA-SEIKRAPF-FNVTY 109
DB 300 PGASVYTRHCSLPEPESAHQSQYTVSVK-----HLEQGRKIMSYNIOMEPTLNLTK 353
QY 110 TFGQYNISWRSDYEDPAFYMLKG-LQYELQYRNKGDPAVSPRRKLISVRSVSLPL 169
DB 354 N-RDSYSLHHEQTKMAYSL-----EHTFQYQYKKKSDSDESKTENLRAHSMDSL 404
QY 170 EPRKDSYELQYRAGPMGSSYQGTWSEMDSPVIFQTO 206
DB 405 QLEPDTSYCARVVKPI--SNYDGIWSKSEBYTKWT 439

RESULT 3
LEPR_MOUSE STANDARD; PRT; 1162 AA.
ID LEPR_MOUSE STANDARD; PRT; 1162 AA.
AC P48356; O35686; Q61215; Q64309; O54986;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Leptin receptor precursor (LEP-R) (OB-R) (B219
DE receptor).
GN LEPR OR OBR OR DB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (VARIANT A).
RX TISSUE-Choroid plexus;
RX MEDLINE=96128129; PubMed=8548812;
RA Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J.,
RA Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,
RA Mitr C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,
RA Mays G.G., Woolf E.A., Montoe C.A., Tepper R.I.;
RT "Identification and expression cloning of a leptin receptor, OB-R";
Cell 83:1263-1271(1995).
RN [2]
RP SEQUENCE FROM N.A. (VARIANT B).
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=96190816; PubMed=8608603;
RA Chen H., Charlat O., Tartaglia L.A., Woolf E.A., Weng X.,
RA Ellis G.M., Lakey N.D., Culpepper J., Moore K.J., Breitbart R.E.,
RA Duyk G.M., Tepper R.I., Morgenstern J.P.;
RT "Evidence that the diabetes gene encodes the leptin receptor:
RT identification of a mutation in the leptin receptor gene in db/db

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RT mice.";
 RL Cell 84:491-495(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (VARIANTS A TO E).
 RC STRAIN=C57BL/6J; TISSUE=HYPOTHALAMUS;
 RX MEDLINE=96231997; PubMed=8628397;
 RA Lee G.-H., Ploence R., Montez J.M., Carroll K.M., Darvishzadeh J.G.,
 RT Lee J.I., Friedman J.M.;
 "Abnormal splicing of the leptin receptor in diabetic mice.";
 RL Nature 379:632-635(1996).
 RN [4]
 RP SEQUENCE FROM N.A. (VARIANT C).
 RC STRAIN=BA1B/C; TISSUE=LIVER;
 RX MEDLINE=96206286; PubMed=8616721;
 RA Cioffi J.A., Shafter A.W., Zupancic T.J., Smith-Gbur J.,
 RT Mikhail A., Platika D., Snodgrass H.R.;
 "Novel B219/OB receptor isoforms: possible role of leptin in
 hemopoiesis and reproduction.";
 RT Nat. Med. 2:585-589(1996).
 RN [5]
 RP SEQUENCE FROM N.A. (VARIANT B).
 RC STRAIN=NEW ZEALAND OBESE / NZO; TISSUE=HYPOTHALAMUS;
 RX MEDLINE=97462708; PubMed=9322935;
 RA Igel M., Becker W., Herberg L., Joost H.G.;
 RT "Hyperleptinemia, leptin resistance, and polymorphic leptin receptor
 in the New Zealand obese mouse.";
 RL Endocrinology 138:4234-4239(1997).
 RN [6]
 RP SEQUENCE FROM N.A. (VARIANTS A AND B).
 RC STRAIN=FVB/N; TISSUE=Spleen;
 RX MEDLINE=96270520; PubMed=8692797;
 RA Ghilardi N., Ziegler S., Westner A., Stoffel R., Helm M.H.,
 RT Skoda R.C.;
 "Defective STAT signalling by the leptin receptor in diabetic mice.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:6231-6235(1996).
 RN [7]
 RP SEQUENCE FROM N.A. (VARIANT E).
 RC STRAIN=129/J;
 RX MEDLINE=98008913; PubMed=9344648;
 RA Chua S.C., Koutiras I.K., Han L., Liu S.M., Kay J., Young S.J.,
 RT Chung W.K., Leibel R.L.;
 "Fine structure of the murine leptin receptor gene: splice site
 suppression is required to form two alternatively spliced
 transcripts.";
 RL Genomics 45:264-270(1997).
 CC -1- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).
 CC -1- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN
 CC TO THE CEREBROSPINAL FLUID. THE PUTATIVE SOLUBLE RECEPTOR (VARIANT
 CC E) COULD FUNCTION AS A TRANSPORT PROTEIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E
 CC WHICH COULD BE SECRETED.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: A, B (SHOWN HERE), C, D AND E;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: (1) VARIANT A: HIGHEST LEVEL OF EXPRESSION IN
 CC LUNG AND KIDNEY, ALSO PRESENT IN CHOROID PLEXUS AND HYPOTHALAMUS.
 CC (2) VARIANT B: HIGHEST LEVEL OF EXPRESSION IN HYPOTHALAMUS AND
 CC LOWER LEVEL IN BRAIN, TESTES AND ADIPOSE TISSUE. (3) VARIANT E:
 CC EXPRESSED IN ADIPOSE TISSUE, HYPOTHALAMUS, HEART, AND TESTES.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC -----
 CC EMBL; U42467; AAA93014.1; -
 CC EMBL; U46135; AAC52408.1; -
 CC EMBL; U49106; AAC52420.1; -
 CC EMBL; U49107; AAC52421.1; -

DR EMBL; U49108; AAC52422.1; -
 DR EMBL; U49109; AAC52423.1; -
 DR EMBL; U49110; AAC52424.1; -
 DR EMBL; U52915; AAC52599.1; -
 DR EMBL; Y10298; CAA71343.1; -
 DR EMBL; U58861; AAC52705.1; -
 DR EMBL; U58862; AAC52706.1; -
 DR EMBL; U58863; AAC52707.1; -
 DR EMBL; AF039456; AAB95334.1; -
 DR EMBL; AF039443; AAB95334.1; JOINED.
 DR EMBL; AF039444; AAB95334.1; JOINED.
 DR EMBL; AF039445; AAB95334.1; JOINED.
 DR EMBL; AF039446; AAB95334.1; JOINED.
 DR EMBL; AF039447; AAB95334.1; JOINED.
 DR EMBL; AF039448; AAB95334.1; JOINED.
 DR EMBL; AF039449; AAB95334.1; JOINED.
 DR EMBL; AF039450; AAB95334.1; JOINED.
 DR EMBL; AF039451; AAB95334.1; JOINED.
 DR EMBL; AF039452; AAB95334.1; JOINED.
 DR EMBL; AF039453; AAB95334.1; JOINED.
 DR EMBL; AF039454; AAB95334.1; JOINED.
 DR EMBL; AF039455; AAB95334.1; JOINED.
 DR HSSP; P40189; IBQU.
 DR MCD; MG1:104993; Lepr.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003961; FM.III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR Pfam; Pf00041; fn3; 3.
 DR SMART; SM00060; FN3; 3.
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
 DR Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KW Polymorphism; Alternative splicing.
 KW SIGNAL
 FT 1 21
 FT CHAIN 22 1162
 FT DOMAIN 22 839
 FT TRANSMEM 840 860
 FT DOMAIN 861 1162
 FT DOMAIN 236 318
 FT DOMAIN 535 621
 FT DOMAIN 736 821
 FT CARBOHYD 41 41
 FT CARBOHYD 56 56
 FT CARBOHYD 73 73
 FT CARBOHYD 98 98
 FT CARBOHYD 187 187
 FT CARBOHYD 275 275
 FT CARBOHYD 345 345
 FT CARBOHYD 431 431
 FT CARBOHYD 514 514
 FT CARBOHYD 622 622
 FT CARBOHYD 657 657
 FT CARBOHYD 668 668
 FT CARBOHYD 686 686
 FT CARBOHYD 695 695
 FT CARBOHYD 698 698
 FT CARBOHYD 726 726
 FT CARBOHYD 890 894
 FT CARBOHYD 895 1162
 FT VARSPLIC 890 892
 FT VARSPLIC 893 1162
 FT VARSPLIC 890 900
 FT VARSPLIC 901 1162
 FT VARSPLIC 797 805
 FT VARSPLIC 806 1162
 FT VARSPLIC 541 541
 FT VARSPLIC 651 651
 FT VARSPLIC 1044 1044
 FT VARSPLIC 140 140
 FT VARSPLIC 720 720
 FT SEQUENCE 1162 AA; 130788 MW; 0E1E75B076BA60A2 CRC64;
 D).
 MISSING (IN THE ISOFORM D).
 DNEPIRYK -> GMCVLPMED (IN ISOFORM E).
 MISSING (IN ISOFORM E).
 V -> I (IN STRAIN NOZ).
 V -> I (IN STRAIN NOZ).
 T -> I (IN STRAIN NOZ).
 A -> I (IN REF. 5).
 F -> T (IN REF. 6).
 MISSING (IN ISOFORM C).
 PETEFLPTH -> DISHEVFLFR (IN ISOFORM
 D).

Query Match 12.1%; Score 144; DB 1; Length 1162;
 Best Local Similarity 31.1%; Pred. No. 5,6e-05;
 Matches 57; Conservative 22; Mismatches 60; Indels 44; Gaps 11;

39 LRKE-----ATSCGSHRSANNAHTATYTCMDYF-----FMADDIFSVNITDGSNGNS 87
 177 LKSFQVQVNCNSLRG-----ECHVPPRAKLANALMLYETTSAGVSFQSPPLMS 227
 88 QECGSELLAESIRPAPP--FNVTYTFSGQYNISWRSDYEDPAFYMLKGLQYELQYRNRG 145
 228 LQ--PMLV---VKDPDPLGLHMEVTDGMLKISMDSQTWAPF-----PLAYQVXKLENS 276
 146 DPAVSRKRLIVSDRSV-SLLPLEFRKDSYELQVRAQPMGSSYQCTSEMSDPYIF 204
 277 T--TVRAEATVATSLVDVSLP-----GSSTEVQVNRKRLDGS--GWSWSSDPQVF 326

QY 205 QTVQ 207
 DB 327 TTQ 329

RESULT 4
 ID IL2B_MOUSE STANDARD; PRT; 539 AA.

AC P16297;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Interleukin-2 receptor beta chain precursor (IL-2 receptor) (P70-75)
 DE (High affinity IL-2 receptor beta subunit) (CD122).
 GN IL2RB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=90175385; PubMed=2155425;
 RA Kono T., Doi T., Yamada G., Hatakeyama M., Minamoto S., Tsuda M.,
 RA Miyazaki M., Miyata T., Taniguchi T.;
 RT "Murine interleukin 2 receptor beta chain: dysregulated gene
 expression in lymphoma line EL-4 caused by a promoter insertion.";
 RT Proc. Natl. Acad. Sci. U.S.A. 87:1806-1810(1990).
 CC
 CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2. THIS BETA SUBUNIT IS
 INVOLVED IN RECEPTOR MEDIATED ENDOCYTOSIS AND TRANSDUCES THE
 MITOGENIC SIGNALS OF IL-2.
 CC
 CC -1- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
 EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
 AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
 CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
 WITH A GAMMA CHAIN.
 CC
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC
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 or send an email to license@sib-sib.ch).
 CC
 CC EMBL: M28052; AAA39283.1; -
 DR PTR: A35052; A35052.
 DR HSSP: P14784; 11LN.
 DR MGD: MGI:96530; 11Ztb.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 1.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
 DR Receptor; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 26
 FT CHAIN 27 539
 FT DOMAIN 27 240
 FT TRANSSEM 241 268
 FT DOMAIN 269 539
 FT DISULFID 36 46
 FT CARBOHYD 74 86
 FT CARBOHYD 30 30
 FT CARBOHYD 43 43
 FT CARBOHYD 55 55
 FT CARBOHYD 71 71
 FT CARBOHYD 150 150
 FT CARBOHYD 216 216
 SO SEQUENCE 539 AA; 60538 MM; 365C9D20686BE14 CR64;

Query Match 11.8%; Score 141.5; DB 1; Length 539;
 Best Local Similarity 22.5%; Pred. No. 3,6e-05;
 Matches 54; Conservative 43; Mismatches 86; Indels 57; Gaps 12;

QY 1 CPDLVCTDYLTQYVICTLEMMNLHPSTLTITWODQYELKDEATSCGSHRSANNAHTATY 60
 DB 31 CSHLECFYNSRANVSC---MWS--HEALNV-----TTCVHAKS-NLRHMK 72
 QY 61 TCHMDVPH-----FMADDIFSVNIT--DQSGNYSOCGSEFLAESIK 100
 DB 73 TCCELTVRAQSMACNLLIGSFPSQSILSYDLIDINVCMEEGMRVKTCDHFPPDNR 132
 QY 101 PAPPFNVTYTF--SGQYNISWR---SDYEDPAFYMLKGLQYELQYRNRGDPVAVSPR 154
 DB 133 LVAPHSLQVLAHIDPQRNCNISMKVSQVSHYTEP-----YLEEFAARRLLGHSWEDA-- 182
 QY 155 KLIVSDRSVSLPLEFRKDSYELQVRAQPMGSSYQCTSEMSDPYIFQVQ--SEELKE 213
 DB 183 SVSLKRRQGMFLFEMLIPSTSYEVQVRYKQAKRNNI--GWSWSPQPLFFRRPADPMKE 240

RESULT 5
 ID TPOR_HUMAN STANDARD; PRT; 635 AA.

AC P40238;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thrombopoietin receptor precursor (TPO-R) (Myeloproliferative leukemia
 protein) (C-mpl) (CD110 antigen).
 GN MPL OR TPOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_TaxID=9606;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=92302297; PubMed=1608974;
 RA Vigon I., Morron J.-P., Cocault L., Mitjavila M.-T., Tambourin P.,
 RA Gisselbrecht S., Souvri M.;
 RT "Molecular cloning and characterization of MPL, the human homolog of
 the v-mpl oncogene. Identification of a member of the hematopoietic
 growth factor receptor superfamily.";
 RT Proc. Natl. Acad. Sci. U.S.A. 89:5640-5644(1992).
 CC
 CC EMBL: M28052; AAA39283.1; -
 DR PTR: A35052; A35052.
 DR MGD: MGI:96530; 11Ztb.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 1.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
 DR Receptor; Transmembrane; Glycoprotein; Signal.

CC CELLS OF HEMATOPOIETIC ORIGIN. THE TWO FORMS (C-MPL-K AND C-MPL-P) ARE ALWAYS FOUND TO BE COEXPRESSED.

CC -1- DISEASE: DEFECTS IN MPL ARE A CAUSE OF CONGENITAL AMEGAKARYOCYTIC THROMBOCYTOPENIA (CAMT); A DISEASE CHARACTERIZED BY ISOLATED THROMBOCYTOPENIA AND MEGAKARYOCYTOPENIA WITH NO PHYSICAL ANOMALIES.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -1- SIMILARITY: CONTAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.

CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-8 IS THE INITIATOR.

CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD110 entry;

CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/11586825.g.htm".

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DR EMBL: M90102; AAA69971.1; -

DR EMBL: M90103; AAA69972.1; -

DR EMBL: U68162; AAB08424.1; -

DR EMBL: U68159; AAB08424.1; JOINED.

DR EMBL: U68160; AAB08424.1; JOINED.

DR EMBL: U68161; AAB08424.1; JOINED.

DR PIR: A45266; A45266.

DR HSSP: P19235; 1EBA.

DR MIM: 159530; -

DR MIM: 604498; -

DR InterPro: IPR002936; CRIA.

DR InterPro: IPR003961; FN.III.

DR InterPro: IPR003528; Hematopo_receptor_L.FI.

DR Pfam: PF00041; fn3; 2.

DR SMART: SM00060; FN3; 2.

DR PROSITE: PS01352; HEMATOPO_REC_L.FI; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing; Repeat; Antigen; Polymorphism.

KW SIGNAL: 1 25 POTENTIAL.

FT CHAIN: 26 635 THROMBOPOIETIN RECEPTOR.

FT DOMAIN: 26 491 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM: 492 513 POTENTIAL.

FT DOMAIN: 514 635 CYTOPLASMIC (POTENTIAL).

FT DISULFID: 40 50 BY SIMILARITY.

FT DISULFID: 77 93 BY SIMILARITY.

FT DISULFID: 291 301 BY SIMILARITY.

FT DISULFID: 323 334 BY SIMILARITY.

FT CARBOHYD: 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD: 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD: 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD: 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARSPLIC: 523 579 RLRHLMPSLPLDLHRLVGLUTLALSPKATVSTCEV EPLSLLEPKSSEKTP -> YPRQAGDMRWKTSWCKQA FLVRSVTPDLRPPVRYGFLPALRHLMDSPLRLTL (IN ISOFORM C-MPL-P).

FT VARSPLIC: 580 635 MISSING (IN ISOFORM C-MPL-P).

FT VARIANT: 58 58 A -> V (IN DBSNP:6087).

FT VARIANT: 168 168 E -> K (IN DBSNP:6088).

FT SEQUENCE: 635 AA: 71244 MW: D25D8D93939DDC CRC64;

Query Match 11.6%; Score 139; DB 1; Length 635;
Best Local Similarity 24.0%; Pred. No. 7.3e-05;
Matches 59; Conservative 25; Mismatches 76; Indels 86; Gaps 14;

QY 4 LNCYDTYDTVCILEMNLHSTLTLMWOQYELKREARSCSL-HRSHNHNATHTY-60
DB 289 LQCTYLDLKNVTC-----QWQDQ-----DHASSQGFYHSRRCCPRDRP 329
QY 61 -----TCHM-----DVFFHMADDFISVNTDOSNYSGSGS-F 93

DB 330 IWENCEEERKNTPGLOTQPSRCHFRKSNDSIIHIL-----VEVTTAPGTAVHSYSGSPF 383

QY 94 LNAESIK-PAPPENYVTFSGOYNISMRSDYEDPAFMLKGLQYLOYRNRG-DPAWVS 151
DB 384 WIGQAVRLPTPLNHRREISGHLLEW---QHPSWNAQ-ENCYQRYRGEGHQWVKV- 437

QY 152 PRKRLLSVSRKSVSLP-----LEFRKDSSELYOVRAGPMPGSSYQCTWSEMSDPYI 203
DB 438 -----LEPLGANGTLELRPSRYRLQURA-RLNGPYQGPWSSMDPYR 482

QY 204 FQFQSE 209
DB 483 VETATE 488

RESULT 6
LEPR_RAT STANDARD; PRT; 1162 AA.
ID Q62959; Q63007; P70493; P70494; Q63385; Q63386; Q54805;
AC P97589; Q35772;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).
GN LEP-R OR OBR OR FA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT B).
RC STRAIN-ZUCKER: TISSUE=Hypothalamus;
RX MEDLINE=96241565; PubMed=8673096;
RA Phillips M.S., Lin Q., Hammond H.A., Dugan V., Hey P.J., Caskey C.T., Hess J.F.;
RT "Leptin receptor missense mutation in the fatty Zucker rat.";
RL Nat. Genet. 13:18-19(1996).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT B).
RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY; TISSUE=Brain;
RX MEDLINE=96295531; PubMed=8702432;
RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
RT "Substitution at codon 269 (glutamine -> proline) of the leptin receptor (OB-R) cDNA is the only mutation found in the Zucker fatty (fa/fa) rat.";
RL Biochem. Biophys. Res. Commun. 224:597-604(1996).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANTS A; B AND E).
RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY;
RX MEDLINE=96332408; PubMed=8769097;
RA Takaya K., Ogawa Y., Isse N., Okazaki T., Satoh N., Masuzaki H., Mori K., Tamura N., Hosoda K., Nakao K.;
RT "Molecular cloning of rat leptin receptor isoform complementary DNAs - identification of a missense mutation in Zucker fatty (fa/fa) rats.";
RL Biochem. Biophys. Res. Commun. 225:75-83(1996).
RN [4]
RP SEQUENCE FROM N.A. (VARIANT B).
RA Karlsson C., Lindell K., Robinson I.C.A.F., Carlsson L.M.S., Carlsson B.;
RT "Cloning of the rat leptin receptor.";
RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT A).
RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY;
RX MEDLINE=96212906; PubMed=8630068;
RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
RT "Phenotype-linked amino acid alteration in leptin receptor cDNA from Zucker fatty (fa/fa) rat.";
RL Biochem. Biophys. Res. Commun. 222:19-26(1996).
RN [6]
RP SEQUENCE OF 1-123 FROM N.A.
RA Morishita T., Hidaka T., Kuzuyama T., Noguchi T.;

RT "Analysis of rat leptin receptor gene."
 RL Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 694-878 FROM N.A.
 RC SPRAIN-SPRAGUE-DAWLEY; TISSUE-Pancreas;
 RA Ma Z.;
 RT "Identification of a leptin receptor in islet."
 RL Submitted (AUG-1996) to the EMBL/Genbank/DBJ databases.
 RN [8]
 RP SEQUENCE OF 843-892 FROM N.A. (VARIANT C).
 RC SPRAIN-SPRAGUE-DAWLEY;
 RA Chien E.K., Hara M., Rouard M., Yano H., Philippe M., Polonsky K.S.,
 RL Bell G.I.;
 RN Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.
 RP VARIANT PA PRO-269
 RX MEDLINE-96314329; PubMed-8690163;
 RA Chua S.C. Jr., White D.W., Wu-Peng X.S., Liu S.M., Okada N.,
 RA Kershaw E.E., Chung W.K., Power-Kehoe L., Chua M., Tartaglia L.A.,
 RA Leibel R.L.;
 "Phenotype of fatty due to Glut29Pro mutation in the leptin receptor
 (Lepr).";
 CC Diabetes 45:1141-1143(1996).
 CC -1- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).
 CC -1- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN
 CC TO THE CEREBROSPINAL FLUID. THE PUTATIVE SOLUBLE RECEPTOR (VARIANT
 CC E) COULD FUNCTION AS A TRANSPORT PROTEIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E
 CC WHICH COULD BE SECRETED.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; A, B (SHOWN HERE), C, D AND E;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- DISEASE: THE FATTY (FA) MUTATION PRODUCES PROFOUND OBESITY OF
 CC EARLY ONSET CAUSED BY HYPERPHAGIA, DEFECTIVE NONSHYERING
 CC THERMOGENESIS, AND PREFERENTIAL DEPOSITION OF ENERGY INTO ADIPOSE
 CC TISSUE.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: U52966; AAC52587.1; -
 DR EMBL: D84350; BAA12697.1; -
 DR EMBL: D84551; BAA12698.1; -
 DR EMBL: D85557; BAA12830.1; -
 DR EMBL: D85558; BAA12831.1; -
 DR EMBL: D85559; BAA12832.1; -
 DR EMBL: U60151; AAB06616.1; -
 DR EMBL: D84125; BAA12230.1; -
 DR EMBL: D84126; BAA12231.1; -
 DR EMBL: AB011006; BAA24899.1; -
 DR EMBL: U67207; AAB40654.1; -
 DR EMBL: AF007818; AAB63201.1; -
 DR InterPro: IPR002996; CRAA.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR Pfam: PF00041; fn3; 2.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
 KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KW Polymorphism; Alternative splicing.
 FT SIGNAL 1 21
 FT CHAIN 22 1162
 FT DOMAIN 22 839
 FT TRANSMEM 840 860
 FT DOMAIN 861 1162
 FT DOMAIN 236 318
 FT DOMAIN 535 621
 FT DOMAIN 736 821

FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 345 345 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 514 514 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 657 657 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 668 668 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 686 686 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 695 695 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 698 698 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 726 726 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 890 894 MISSING (IN ISOFORM A).
 FT VARSPLIC 895 892 PET -> VTV (IN ISOFORM A).
 FT VARSPLIC 893 1162 MISSING (IN ISOFORM C).
 FT VARSPLIC 797 805 DNFIPIEKY -> GMCTVLLLN (IN ISOFORM E).
 FT VARSPLIC 806 1162 MISSING (IN ISOFORM E).
 FT VARIANT 269 269 Q -> P (IN FA).
 FT CONFLICT 2 2 T -> M (IN REF. 4).
 FT CONFLICT 12 12 H -> P (IN REF. 6).
 FT CONFLICT 34 34 K -> R (IN REF. 6).
 FT CONFLICT 751 752 CV -> SL (IN REF. 7).
 FT CONFLICT 846 846 I -> V (IN REF. 8).
 SQ SEQUENCE 1162 AA; 130832 MM; BA7AC20A2D2E62AF CRC64;
 Query Match 11.5%; Score 138; DB 1; Length 1162;
 Best Local Similarity 30.9%; Pred. No. 0.00019;
 Matches 56; Conservative 23; Mismatches 62; Indels 40; Gaps 11;
 QY 39 LKD-EATSCSLHRSANHTATYTCCHMDYR-----FNADIFSVNTTDDSGNYSOE 89
 DB 177 LKSFQVQC-----NCSVRECECHVPPRAKYNVALMYLETITAGVSFSPMSIQ 229
 QY 90 CGSFLAESIKPAP--FNVTVTFSGOYNISWRSPDEDPAFYMLKGLQYLRNRGDP 147
 DB 230 --PLTV---VKPPPLGLRMEVTDGNNLKISWDSQKAPF-----PLYQVYLRNST- 277
 QY 148 WAYSFRKLISYDSRSV-SILPLEFRKDSYELQVRASPMGSSYOGTSWSPDPVIFOT 206
 DB 278 -IYREAAEIVSDTSLYDSVLP-----GSSYEVQYRKRLDGS--GWSDMSLPOLFTT 328
 QY 207 Q 207
 DB 329 Q 329
 RESULT 7
 LEPR_HUMAN STANDARD; PRT; 1165 AA.
 AC P48357;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Leptin receptor precursor (LEP-R) (OB receptor) (OB-R).
 GN LEPR OR OBR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE-96128129; PubMed-8548812;
 RA Tartaglia L.A., Dembski M., Meng X., Deng N., Culpepper J.,
 RA Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,
 RA Mufir C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,

DB	Query Match	Best Local Similarity	Matches	Score	DB 1:	Length	DB 2:	Score	DB 3:	Length	DB 4:	Score	DB 5:	Length	DB 6:	Score	DB 7:	Length	DB 8:	Score	DB 9:	Length	DB 10:	Score	DB 11:	Length	DB 12:	Score	DB 13:	Length	DB 14:	Score	DB 15:	Length	DB 16:	Score	DB 17:	Length	DB 18:	Score	DB 19:	Length	DB 20:	Score	DB 21:	Length	DB 22:	Score	DB 23:	Length	DB 24:	Score	DB 25:	Length	DB 26:	Score	DB 27:	Length	DB 28:	Score	DB 29:	Length	DB 30:	Score	DB 31:	Length	DB 32:	Score	DB 33:	Length	DB 34:	Score	DB 35:	Length	DB 36:	Score	DB 37:	Length	DB 38:	Score	DB 39:	Length	DB 40:	Score	DB 41:	Length	DB 42:	Score	DB 43:	Length	DB 44:	Score	DB 45:	Length	DB 46:	Score	DB 47:	Length	DB 48:	Score	DB 49:	Length	DB 50:	Score	DB 51:	Length	DB 52:	Score	DB 53:	Length	DB 54:	Score	DB 55:	Length	DB 56:	Score	DB 57:	Length	DB 58:	Score	DB 59:	Length	DB 60:	Score	DB 61:	Length	DB 62:	Score	DB 63:	Length	DB 64:	Score	DB 65:	Length	DB 66:	Score	DB 67:	Length	DB 68:	Score	DB 69:	Length	DB 70:	Score	DB 71:	Length	DB 72:	Score	DB 73:	Length	DB 74:	Score	DB 75:	Length	DB 76:	Score	DB 77:	Length	DB 78:	Score	DB 79:	Length	DB 80:	Score	DB 81:	Length	DB 82:	Score	DB 83:	Length	DB 84:	Score	DB 85:	Length	DB 86:	Score	DB 87:	Length	DB 88:	Score	DB 89:	Length	DB 90:	Score	DB 91:	Length	DB 92:	Score	DB 93:	Length	DB 94:	Score	DB 95:	Length	DB 96:	Score	DB 97:	Length	DB 98:	Score	DB 99:	Length	DB 100:	Score	DB 101:	Length	DB 102:	Score	DB 103:	Length	DB 104:	Score	DB 105:	Length	DB 106:	Score	DB 107:	Length	DB 108:	Score	DB 109:	Length	DB 110:	Score	DB 111:	Length	DB 112:	Score	DB 113:	Length	DB 114:	Score	DB 115:	Length	DB 116:	Score	DB 117:	Length	DB 118:	Score	DB 119:	Length	DB 120:	Score	DB 121:	Length	DB 122:	Score	DB 123:	Length	DB 124:	Score	DB 125:	Length	DB 126:	Score	DB 127:	Length	DB 128:	Score	DB 129:	Length	DB 130:	Score	DB 131:	Length	DB 132:	Score	DB 133:	Length	DB 134:	Score	DB 135:	Length	DB 136:	Score	DB 137:	Length	DB 138:	Score	DB 139:	Length	DB 140:	Score	DB 141:	Length	DB 142:	Score	DB 143:	Length	DB 144:	Score	DB 145:	Length	DB 146:	Score	DB 147:	Length	DB 148:	Score	DB 149:	Length	DB 150:	Score	DB 151:	Length	DB 152:	Score	DB 153:	Length	DB 154:	Score	DB 155:	Length	DB 156:	Score	DB 157:	Length	DB 158:	Score	DB 159:	Length	DB 160:	Score	DB 161:	Length	DB 162:	Score	DB 163:	Length	DB 164:	Score	DB 165:	Length	DB 166:	Score	DB 167:	Length	DB 168:	Score	DB 169:	Length	DB 170:	Score	DB 171:	Length	DB 172:	Score	DB 173:	Length	DB 174:	Score	DB 175:	Length	DB 176:	Score	DB 177:	Length	DB 178:	Score	DB 179:	Length	DB 180:	Score	DB 181:	Length	DB 182:	Score	DB 183:	Length	DB 184:	Score	DB 185:	Length	DB 186:	Score	DB 187:	Length	DB 188:	Score	DB 189:	Length	DB 190:	Score	DB 191:	Length	DB 192:	Score	DB 193:	Length	DB 194:	Score	DB 195:	Length	DB 196:	Score	DB 197:	Length	DB 198:	Score	DB 199:	Length	DB 200:	Score	DB 201:	Length	DB 202:	Score	DB 203:	Length	DB 204:	Score	DB 205:	Length	DB 206:	Score	DB 207:	Length	DB 208:	Score	DB 209:	Length	DB 210:	Score	DB 211:	Length	DB 212:	Score	DB 213:	Length	DB 214:	Score	DB 215:	Length	DB 216:	Score	DB 217:	Length	DB 218:	Score	DB 219:	Length	DB 220:	Score	DB 221:	Length	DB 222:	Score	DB 223:	Length	DB 224:	Score	DB 225:	Length	DB 226:	Score	DB 227:	Length	DB 228:	Score	DB 229:	Length	DB 230:	Score	DB 231:	Length	DB 232:	Score	DB 233:	Length	DB 234:	Score	DB 235:	Length	DB 236:	Score	DB 237:	Length	DB 238:	Score	DB 239:	Length	DB 240:	Score	DB 241:	Length	DB 242:	Score	DB 243:	Length	DB 244:	Score	DB 245:	Length	DB 246:	Score	DB 247:	Length	DB 248:	Score	DB 249:	Length	DB 250:	Score	DB 251:	Length	DB 252:	Score	DB 253:	Length	DB 254:	Score	DB 255:	Length	DB 256:	Score	DB 257:	Length	DB 258:	Score	DB 259:	Length	DB 260:	Score</
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OY 161 SRV-SLLPFRKDSYELQVAGPMPGSSYOGTWSWSDPIYRQ 207
 DB 292 SLVSDILP-----GSSYEVQKGRKLDG---PQINSMDSTPRVFTQ 331

RESULT 8
 IL4R_HUMAN STANDARD: PRT; 825 AA.
 AC P24394;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Interleukin-4 receptor alpha chain precursor (IL-4R-alpha) (CD124 antigen)
 GN IL4R OR IL4RA OR 582J2.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 SEQUENCE FROM N.A.
 TISSUE=peripheral blood;
 MEDLINE=90171849; PubMed=2307934;
 RA Idzerda R.L., March C.J., Mosley B., Lyman S.D., Bos T.V., Gimpel S.D., Din W.S., Grabstein K.H., Wildmer M.B., Park L.S., Cosman D., Beckmann M.P.;
 RA "Human interleukin 4 receptor confers biological responsiveness and defines a novel receptor superfamily.";
 RT J. Exp. Med. 171:861-873(1990).
 RL [2]
 SEQUENCE FROM N.A.
 MEDLINE=91120547; PubMed=2278997;
 RA Gallizzi J.-P., Zuber C.E., Harada N., Gorman D.M., Djossou O., Kastelein R., Banchereau J., Howard M., Miyajima A.;
 RA "Molecular cloning of a cDNA encoding the human interleukin 4 receptor.";
 RT Int. Immunol. 2:669-675(1990).
 RL [3]
 SEQUENCE FROM N.A.
 MEDLINE=99425270; PubMed=10493829;
 RA Loftus B.J., Kim U.-T., Sneedon V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Diehlert E.E., Harris P.C., Venter J.C., Adams M.D.;
 RA "Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";
 RT Genomics 60:295-308(1999).
 RL [4]
 VARIANTS VAL-75; ALA-400; ARG-431; LEU-436 AND PRO-786.
 MEDLINE=97224413; PubMed=9070874;
 RA Deichmann K., Bardutzky J., Forster J., Heinemann A., Kuehr J.;
 RA "Common polymorphisms in the coding part of the IL4-receptor gene.";
 RT Biochem. Biophys. Res. Commun. 231:696-697(1997).
 RL [5]
 VARIANT ATOPIC ARG-576.
 MEDLINE=98041803; PubMed=9392697;
 RA Hershley G.K.K., Friedrich M.F., Esswein L.A., Thomas M.L., Chatilla T.A.;
 RA "The association of atopy with a gain-of-function mutation in the alpha subunit of the interleukin-4 receptor.";
 RT New Engl. J. Med. 337:1720-1725(1997).
 RL [6]
 VARIANT ATOPIC ASTHMA VAL-75.
 MEDLINE=98282087; PubMed=9620765;
 RA Mitsuyasu H., Izuhara K., Mao X.-O., Gao P.S., Arihara Y., Enomoto T., Kawai M., Sasaki S., Dake Y., Hamagaki N., Shirakawa T., Hopkin J.M.;
 RA "H505val variant of IL4R alpha upregulates Ige synthesis and associates with atopic asthma.";
 RT Nat. Genet. 19:119-120(1998).
 RL [7]
 VARIANT ATOPIC ASTHMA VAL-75.
 MEDLINE=99322293; PubMed=10390422;

RA Noguchi E., Shibasaki M., Ariuami T., Takeda K., Yokouchi Y., Kobayashi K., Imoto N., Nakahara S., Matsui A., Hamaguchi H.;
 RA "No association between atopy/asthma and the H505val polymorphism of IL-4 receptor.";
 RT Am. J. Respir. Crit. Care Med. 160:342-345(1999).
 RL [8]
 VARIANTS PRO-503 AND ARG-576.
 MEDLINE=99250314; PubMed=10233717;
 RA Kruse S., Japha T., Tedner M., Sparholt S.H., Forster J., Kuehr J., Deichmann K.A.;
 RA "The polymorphisms 5503p and Q576R in the interleukin-4 receptor alpha gene are associated with atopy and influence the signal transduction.";
 RT Immunology 96:365-371(1999).
 RL [9]
 VARIANT ALA-752.
 MEDLINE=20143377; PubMed=10677312;
 RA Ober C., Leavitt S.A., Tsalenko A., Howard T.D., Hoki D.M., Daniel R., Newman D.L., Wu X., Parry R., Lester U.A., Solway J., Blumenthal M., King R.A., Xu J., Meyers D.A., Blecker E.R., Cox N.J.;
 RA "Variation in the interleukin 4-receptor alpha gene confers susceptibility to asthma and atopy in ethnically diverse populations.";
 RT Am. J. Hum. Genet. 66:517-526(2000).
 RL [10]
 VARIANT ATOPIC ARG-576.
 MEDLINE=20269830; PubMed=10809862;
 RA Oiso N., Fukai K., Ishii M.;
 RA "Interleukin 4 receptor alpha chain polymorphism Glu551Arg is associated with adult atopic dermatitis in Japan.";
 RT Br. J. Dermatol. 142:1003-1006(2000).
 RL [11]
 VARIANT PRO-786.
 MEDLINE=21405389; PubMed=11513543;
 RA Andrews R.P., Burrell L., Rosa-Rosa L., Cunningham C.M., Brzezinski J.L., Bernstein J.A., Khurana Hershey G.K.;
 RA "Analysis of the Ser786Pro interleukin-4 receptor alpha allelic variant in allergic and nonallergic asthma and its functional consequences.";
 RT Clin. Immunol. 100:298-304(2001).
 RL [12]
 VARIANT ILE-579.
 MEDLINE=21182061; PubMed=11285129;
 RA Lozano F., Peces de la Iglesia A., Miserachs N., Vives J., Valisella S., Suarez E., Lopez de la Iglesia A., Miserachs N., Vives J.;
 RA "Identification of a novel single-nucleotide polymorphism (Val554Ile) and definition of eight common alleles for human IL4RA exon 11.";
 RT Tissue Antigens 57:216-220(2001).
 RL -1- FUNCTION: THIS IS A RECEPTOR FOR INTERLEUKIN-4. A SOLUBLE FORM OF THE IL-4 RECEPTOR MAY REPRESENT A REGULATORY MOLECULE SPECIFIC FOR IL-4-DEPENDENT IMMUNE RESPONSES.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA CHAIN AND A COMMON GAMMA CHAIN.
 CC -1- DISEASE: DEFECTS IN IL4R ARE A CAUSE OF ATOPIC ASTHMA.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME=PRO7; NOTE=CD guide CD124 entry;
 WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd124.htm"
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 CC EMBL: X52425; CAA36672.1; -;
 CC EMBL: AC004525; AAC23495.1; -;
 DR PIR: A60386; A60386.
 DR PIR: A47603; A47603.
 DR MIM: 147781; -;
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.

CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN	NCHI_Taxid-101116;
RX	SEQUENCE FROM N.A.; PubMed-1889461;
RP	MEDLINE-91364784; Page T.H., Dailman M.J.;
RA	"Molecular cloning of cDNAs for the rat interleukin 2 receptor alpha
RT	and beta chain genes: differentially regulated gene activity in
FT	response to mitogenic stimulation.";
RL	Eur J Immunol. 21:2133-2138(1991).
CC	-1. FUNCTION: RECEPTOR FOR INTERLEUKIN-2. THIS BETA SUBUNIT IS
CC	INVOLVED IN RECEPTOR-MEDIATED ENDOCYTOSIS AND TRANSDUCES THE
CC	MITOGENIC SIGNALS OF IL-2R
CC	-1. SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
CC	EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
CC	AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CC	CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
CC	WITH A GAMMA CHAIN.
CC	-1. SUBCELLULAR LOCATION: Type I membrane protein.
CC	-1. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC	-1. This SWISS-PROT entry is copyright. It is produced through a collaborator
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CC	entities requires a license agreement. See http://www.isb-sib.ch/announce/ .
CC	or send an email to license@isb-sib.ch .
CC	EMBL; M55050; AAA41429.1; "
DR	HSSP; P14784; 11LN.
DR	InterPro: IPRO02996; CR1A.
DR	InterPro: IPRO03961; FN.III.
DR	InterPro: IPRO03531; Hematopo_receptor_S.F1.
DR	Pfam; PF00041; fn3; 1.
DR	SMART; SMO0060; FN3; 1.
DR	PROSITE; PS01355; HEMATOPO_REC_SF_1; 1.
KW	Receptor; Transmembrane; Glycoprotein; Signal.
FT	SIGNAL 1 26 POTENTIAL.
FT	CHAIN 27 537 INTERLEUKIN-2 RECEPTOR BETA CHAIN.
FT	DOMAIN 27 239 EXTRACELLULAR (POTENTIAL).
FT	DOMAIN 240 267 POTENTIAL.
FT	DOMAIN 268 537 CYTOPLASMIC (POTENTIAL).
FT	DISULFID 36 46 BY SIMILARITY.
FT	DISULFID 74 86
FT	CARBOHYD 43 (POTENTIAL).
FT	CARBOHYD 53 (POTENTIAL).
FT	CARBOHYD 53 53 N-LINKED (GLCNAC..) (POTENTIAL).
FT	CARBOHYD 71 71 N-LINKED (GLCNAC..) (POTENTIAL).
FT	CARBOHYD 150 150 N-LINKED (GLCNAC..) (POTENTIAL).
SO	SEQUENCE 537 AA; 60657 MW; 9C74A424F361968 CRC64;
Query Match	11.2%; Score 134; DB 1; Length 537;
Best Local Similarity	23.1%; Pred. No. 0.00016;
Matches 58;	Conservative 41; Mismatches 72; Indels 80; Gaps 13
OY	1 CPDLVCYDYLVQVVICILEMNUNHPSHTLTWQDYEELKDEA---TSCSLHSAR--- 53
DB	31 CSHLCPCFYNSRAVNC-----MMS-----PEEALNVTSCHTHAKSPMRHW 70
OY	54 NAT-----HATYTHM-----DVDFHMADDFSVNIT--DOSGANSOECSCFLIARS 98
DB	71 NTCELPVPVRASMACNILLPLPDSSQLTVSDLISTSYCWEEKGMWRBYTCFPHPDFN 130
OY	99 IKRAPPPPVNYTFE--SGQYNISMWR--SDYEDPAFWMLGKLOYELOLYRNRGDPAAVSP 152
DB	131 LRIILAPHSLOYLHIETPRGNINSIMWSGVSHYVN-----YLEEF-----A 170
OY	153 RKRLIVDSRSVSLDLPERK-----DSSEYLOVNRAGMGSSGYCTGSWEUSDV 202
DB	171 RRRLDRSRMEDVASVFSLKRQRMVLETLTPPTSTVELQVYVIAQGSKI--RTSPSPSQPM 228

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QY 203 IPOTOSEBEKE 213
DB 229 AFRTPADPRE 239

RESULT 10
CYRG_MOUSE STANDARD: PRT: 369 AA.
AC P34902;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cytokine receptor common gamma chain precursor (Gamma-C)
DE (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
GN IL2RG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=9327575; PubMed=8503926;
Kumaki S., Kondo M., Takeshita T., Asao H., Nakamura M., Sugamura K.;
"Cloning of the mouse Interleukin 2 receptor gamma chain:
demonstration of functional differences between the mouse and human
receptors."
Biochem. Biophys. Res. Commun. 193:356-363(1993).
RN [2]
SEQUENCE FROM N.A.
STRAIN=CBA/CAI;
MEDLINE=93391374; PubMed=8378320;
Cao X., Kozak C.A., Liu Y.J., Noguchi M., O'Connell E., Leonard W.J.;
"Characterization of cDNAs encoding the murine interleukin 2 receptor
(IL-2R) gamma chain: chromosomal mapping and tissue specificity of
IL-2R gamma chain expression."
Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468(1993).
RN [3]
SEQUENCE FROM N.A.
MEDLINE=9336191; PubMed=8356999;
Kobayashi N., Nakagawa S., Minami Y., Taniguchi T., Kono T.;
"Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
gamma."
Gene 130:303-304(1993).
RN [4]
SEQUENCE FROM N.A.
MEDLINE=95104285; PubMed=7805728;
Disanto J.P., Certain S., Wilson A., Macdonald R.R., Avner P.,
Fischer A., de Saint Basile G.;
"The murine interleukin-2 receptor gamma chain gene: organization,
chromosomal localization and expression in the adult thymus."
Eur. J. Immunol. 24:3014-3016(1994).
RN [5]
SEQUENCE FROM N.A.
STRAIN=B6.S;
MEDLINE=9631745; PubMed=8750189;
Chiu R.K., Droll A., Cooper D.L., Dougherty S.T., Dirks J.F.,
Dougherty G.J.;
"Molecular mechanisms regulating the hyaluronan binding activity of
the adhesion protein CD44."
J. Neurosci. 16:231-239(1995).
RN [6]
FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
INTERLEUKINS.
CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC -1- SUBCELLULAR LOCATION: TYPE I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC or send an email to license@isb.ch).
CC -----
CC EMBL: D13821; BAA02974.1; -
CC EMBL: G21795; AAB4279.1; -
CC EMBL: D13565; BAA02760.1; -
CC EMBL: L20048; AAB39286.1; -
CC EMBL: S75852; AAB32904.1; -
CC EMBL: S75844; AAB32904.1; JOINED.
CC EMBL: S75845; AAB32904.1; JOINED.
CC EMBL: S75847; AAB32904.1; JOINED.
CC EMBL: S75848; AAB32904.1; JOINED.
CC EMBL: S75849; AAB32904.1; JOINED.
CC EMBL: S75850; AAB32904.1; JOINED.
CC EMBL: S75851; AAB32904.1; JOINED.
CC PIR: J00592; CAA53085.1; -
CC PIR: J00775; J00775.
CC HSSP: P31785; 1ILN.
CC MGD: MGI:96551; 1L29.
CC InterPro: IPR002996; CRIA.
CC InterPro: IPR003531; FN.III.
CC Pfam: PF00041; fn3.1.
CC SMART: SM00060; FN3.1.
CC PROSITE: PS01355; HEMATOPO_REC_S_F1.1.
CC Receptor: Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1 22 BY SIMILARITY.
CC CHAIN 23 369 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
CC DOMAIN 23 263 EXTRACELLULAR (POTENTIAL).
CC TRANSEM 264 284 POTENTIAL.
CC DOMAIN 285 369 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 151 250 FIBRONECTIN TYPE-III.
CC DISULFID 62 72 POTENTIAL.
CC DISULFID 102 115 POTENTIAL.
CC CARBOHYD 71 71 N-LINKED (GLCNAc. . .) (POTENTIAL).
CC CARBOHYD 75 75 N-LINKED (GLCNAc. . .) (POTENTIAL).
CC CARBOHYD 84 84 N-LINKED (GLCNAc. . .) (POTENTIAL).
CC CARBOHYD 96 96 N-LINKED (GLCNAc. . .) (POTENTIAL).
CC CARBOHYD 159 159 N-LINKED (GLCNAc. . .) (POTENTIAL).
CC CARBOHYD 164 164 N-LINKED (GLCNAc. . .) (POTENTIAL).
CC SEQUENCE 369 AA; 42241 MW; CB2D5A459077AC7 CRC64;

Query Match 11.2%; Score 133.5; DB: 1; Length 369;
Best Local Similarity 25.28; Pred: No 0.00011;
Matches 56; Conservative 33; Mismatches 94; Indels 39; Gaps 12;

QY 2 PDLYCYTDYLYQVYICLEMN--LHPSTLTLTWQDQYELADEAT--SCGLRSANHTH 57
DB 58 PEVQCFEYFNLEIYNNC--TWNSSEFPQATNLTLYHTV-KVSDNNTPOECHLTFSEITS 113
QY 58 ATVYCHMDVFNHADDIPSVINITDQSGNYSQEGSFLAESIKAPPPVYVT--PSCQY 115
DB 114 G---CQIQKEDIDLYQTFVYVLODPKQFORRAVOKLNQNLVIRAEENTLTSNSESOL 170
QY 116 NISWRSYDEDPAYMLKGR-LQYELQYR-NRGDPVAV-----SPRRKLISVDSRSVSLP 168
DB 171 ELRKSKSH-----IKERCLQYLVQYRSNRDSWTELVNHEFRFLPSVDE----- 216
QY 169 LEFRKDSYELQYRAGPAGSGSYOGTSEMSDPVIFQOSEE 210
DB 217 --LKRYPFRVRSRYNPICGSSD--MSKMSQPVHMGSHIVE 253

RESULT 11
TPOR_MOUSE STANDARD: PRT: 625 AA.
AC Q088351;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thrombopoietin receptor precursor (TPO-R) (Myelopoietic Leukemia

```


DE protein) (C-mpl).
 GN MPL OR TPOR.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93327753; PubMed=8334987;
 RA Skoda R.C., Seldin D.C., Chiang M.K., Peichel C.L., Vogt T.F.,
 RA Leder P.;
 RT "Murine c-mpl: a member of the hematopoietic growth factor receptor
 RT superfamily that transduces a proliferative signal.";
 RL EMBO J. 12:2645-2653(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=ICFW; TISSUE=Fetal liver;
 MEDLINE=93390934; PubMed=8397366;
 RA Vigon I., Florindo C., Fichelson S., Guenet J.-L., Mattei M.-G.,
 RA Souyri M., Cosman D., Gisselbrecht S.;
 RT "Characterization of the murine Mpl proto-oncogene, a member of the
 RT hematopoietic cytokine receptor family: molecular cloning,
 RT chromosomal location and evidence for a function in cell growth.";
 RL Oncogene 8:2607-2615(1993).
 CC -1- FUNCTION: RECEPTOR FOR THROMBOPOIETIN. MAY REPRESENT A REGULATORY
 CC MOLECULE SPECIFIC FOR TPO-R-DEPENDENT IMMUNE RESPONSES.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 CC -----
 DR EMBL: 222649; GAA80365.1; -;
 DR EMBL: 222657; GAA80372.1; -;
 DR EMBL: 273677; GAA52031.1; -;
 DR PIR: S35317; S35317.
 DR HSSP: P19235; IEBA.
 DR MGI: MGI:97076; Mpl.
 DR InterPro: IPR002996; CRLA.
 DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR003528; Hematopo_receptor_L.FI.
 DR Pfam: PF00041; fn3.1.
 DR SMART: SM00060; FN3.1.
 DR PROSITE: PS01352; HEMATOPO_REC_L.FI.1.
 DR Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 25
 FT CHAIN 1 25
 FT DOMAIN 26 625
 FT TRANSMEM 26 482
 FT DOMAIN 483 504
 FT DOMAIN 505 625
 FT CARBOHYD 117 117
 FT CONFLICT 2 8
 FT CONFLICT 99 99
 FT CONFLICT 222 222
 FT SEQUENCE 625 AA; 69817 MW; 309CF6EAA3724549 CRC64;
 SO
 Query Match 11.18; Score 132.5; DB 1; Length 625;
 Best Local Similarity 25.08; Pred. No. 0.00027;
 Matches 60; Conservative 25; Mismatches 80; Indels 75; Gaps 14;
 QY 4 LVCYDYVQYQYILEMMNHPSTLTWQDOYELKDEATSCSLRSANMTHATY-- 61
 DB 281 LQCFPLDKMKWTC-----QWQOQ-----DRSSGGR--HSRRRCPTDR 319
 QY 62 -----CHM-----DVFFHADIIFSVNTTDSGNSQSGCS- 92

DB 320 DPTWEKEEERPRGSPALYSRCHFRKSRNDSVHIL-----VEVTTAQAVHSYLGSP 373
 QY 93 FILAEIST-KPAPEFNVYTFESGQYNISMSRSDYEDPAFYMLKGLQYELQRYNRG-DPMAY 150
 DB 374 FWHQAVLLPPTSLHREVSSGRLELMQHOSSWA-----QETCYQLRYTGEGRDMKV 428
 QY 151 -SPRRKLISVDGRSVSLLEFRKDSSEYLOVRAGPMPGSSYQGTSEMSDPVIFQTOSE 209
 DB 429 LEP-----SLARGST---LELRPRARYSLQLR-RLNGFTYGPMSANSPARVSTGSE 479
 RESULT 12
 CYRG_BOVIN STANDARD; PRT; 379 AA.
 ID CYRG_BOVIN
 AC 095118;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Cytokine receptor common gamma chain precursor (Gamma-C)
 DE (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (p64).
 GN IL2RG.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 CC Bovidae; Bovinae; Bos.
 CX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96268473; PubMed=8672241;
 RA Yoo J., Stone R.T., Solinas-Toldo S., Fries R., Beattie C.W.;
 RT "Cloning and chromosomal mapping of bovine interleukin-2 receptor
 RT gamma gene.";
 RL DNA Cell Biol. 15:453-459(1996).
 CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
 CC INTERLEUKINS.
 CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
 CC PROBABLY ALSO THE IL-13 RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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 CC -----
 DR EMBL: U33748; AAB07812.1; -;
 DR HSSP: P31785; ILIN.
 DR InterPro: IPR002996; CRLA.
 DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR003531; Hematopo_receptor_S.FI.
 DR Pfam: PF00041; fn3.1.
 DR SMART: SM00060; FN3.1.
 DR PROSITE: PS01355; HEMATOPO_REC_S.FI.1.
 DR Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 22
 FT CHAIN 1 379
 FT DOMAIN 23 269
 FT TRANSMEM 270 290
 FT DOMAIN 291 379
 FT DOMAIN 158 256
 FT DISULFID 68 78
 FT DISULFID 109 122
 FT CARBOHYD 77 77
 FT CARBOHYD 81 81
 FT CARBOHYD 90 90
 FT CARBOHYD 166 166
 FT CARBOHYD 171 171
 FT SEQUENCE 379 AA; 43037 MW; 33CFAD9C9B032178 CRC64;
 SO

Query Match 10.7%; Score 127.5; DB 1; Length 379;
 Best Local Similarity 23.5%; Pred. No. 0.0004;
 Matches 53; Conservative 40; Mismatches 102; Indels 31; Gaps 10;

CC 2 PDLCVYDYQVYICILEMWNL-----HPSTLTPLTWODYEELKDEATSCSLHRSANAH 57
 DB 64 PKVCCFVFNVEYMNK---TWNSSSEPRPTNLTHVYKNSND--DKVCEGCHYLFSEVIT 120
 QY 58 ATYTCMDVFEHMADDFSVNITDQSGNYSQECGSPFLAESIKPAPPEVNTVTFSGQ-- 115
 DB 121 G---CWEGKEIRLYETFEVYQDRPREHROKQMLKLDLVIPAPENLTLRLNLSFOL 177
 QY 116 NISWRSDYEDPAFYMLKGLQYELQYR-NRGPMAVSRRKLISVDSR-SVSLPLEFR 173
 DB 178 ELSMSNRHLDC-----LEHLYQYRSDMRQSWTEQ-----SVDRHNSFLSPVDAQ 224
 QY 174 DSSYELQVRAGPMPGSSYOGTSEMSDPYIF--QTQSELEKGNRP 217
 DB 225 LYTFVRNRYNPICGSAQR--WSDMSYPLHMGSTSKENIENPENP 268
 SUIT 13
 CYRG_CANFA STANDARD: PRT: 373 AA.
 AC PA0321:
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Cytokine receptor common gamma chain precursor (Gamma-C)
 DE (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
 GN IL2RG.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=95130114; PubMed=7829104;
 RA Henthorn P.S., Somborg R.L., Pamlani V.M., Puck J.M., Patterson D.F.,
 RA Felsburg P.J.;
 RT "IL-2R gamma gene microdeletion demonstrates that canine X-linked
 RT severe combined immunodeficiency is a homologue of the human
 RT disease";
 RT Genomics 23:69-74(1994).
 RL
 CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
 CC INTERLEUKINS.
 CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
 CC PROBABLY ALSO THE IL-13 RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A CANINE X-LINKED
 CC SEVERE COMBINED IMMUNODEFICIENCY.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC
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 CC
 CC EMBL: U04361; AAC48403.1; -.
 DR HSSP: P31785; IILN.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR003531; Hematopo_receptor_s.fl.
 DR Pfam: PF000041; fn3.1.
 DR SMART: SM00060; FN3.1.
 DR PROSITE: PS01355; HEMATOPO_REC_S_FL; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 22
 FT CHAIN 23 373
 FT DOMAIN 23 261
 FT TRANSMEM 262 283
 FT DOMAIN 284 373
 FT DOMAIN 151 249
 FT DISULFID 62 72
 FT DISULFID 102 115
 FT CARBOHYD 24 24
 FT CARBOHYD 71 71
 FT CARBOHYD 75 75
 FT CARBOHYD 84 84
 FT CARBOHYD 159 159
 FT CARBOHYD 164 164
 FT CARBOHYD 249 249
 SQ SEQUENCE 373 AA; 42516 MW; 03A0DB1F8B08DB8 CRC64;
 Query Match 10.6%; Score 127; DB 1; Length 373;
 Best Local Similarity 24.3%; Pred. No. 0.00043;
 Matches 51; Conservative 35; Mismatches 92; Indels 32; Gaps 11;
 CC 2 PDLCVYDYQVYICILEMWNL-----HPSTLTPLTWODYEELKDEATSCSLHRSANAH 56
 DB 58 PEVCCFVFNVEYMNK---TWNSSSEPRPTNLTHVYKNSND--DKVCEGCHYLFSEVIT 112
 QY 57 HATYTCMDVFEHMADDFSVNITDQSGNYSQECGSPFLAESIKPAPPEVNTVTFSGQ 114
 DB 113 AG---CWQKEEIRLYETFEVYQDRPREHROKQMLKLDLVIPAPENLTLRLNLSFOL 169
 QY 115 NISWRSDYEDPAFYMLKGLQYELQYR-NRGPMAVSRRKLISVDSR-SVSLPLEFR 172
 DB 170 ELSMSNRHLDC-----LEHLYQYRSDMRQSWTEQ-----SVDRHNSFLSPVDAQ 216
 QY 173 KDSYELQVRAGPMPGSSYOGTSEMSDPY 202
 DB 217 KYTFVRNRYNPICGSAQR--WSEMSHP 244
 RESULT 14
 IL2B_HUMAN STANDARD: PRT: 551 AA.
 ID IL2B_HUMAN
 AC P14784;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Interleukin-2 receptor beta chain precursor (IL-2 receptor) (P70-75)
 DE (High affinity IL-2 receptor beta subunit) (CD122 antigen).
 GN IL2RB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89242117; PubMed=2785715;
 RA Hatakeyama M., Tsudo M., Minamoto S., Kono T., Doi T., Miyata T.,
 RA Miyasaka M., Taniguchi T.;
 RT "Interleukin-2 receptor beta chain gene: generation of three receptor
 RT forms by cloned human alpha and beta chain cDNA's";
 RT Science 244:551-556(1989).
 RL
 CC SEQUENCE FROM N.A.
 RX MEDLINE=20057165; PubMed=10591208;
 RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
 RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.,
 RA Baguley C., Bailey J., Barlow K., Bates K.N., Beasley O., Bird C.P.,
 RA Blakey S., Bridgeman A.M., Buck D., Burgess J., Burrill W.D.,
 RA Burton J., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M.,
 RA Cobley V., Cole C.G., Collier R.E., Connor R.E., Conroy D., Corby N.,
 RA Coville G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
 RA Dodsorth S.J., Durbin R.M., Ellington A., Evans K.L., Fey J.M.,
 RA Fleming K., French L., Garner A.A., Gilbert J.G.R., Goward M.E.,

RA Graftsmo D., Griffiths M.N., Hall C., Hall R., Hilt-Tamlyn G.,
RA Heathcote R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J.,
RA Kimberley A., King A., Laird G.K., Langford C.F., Leversha M.A.,
RA Lloyd C., Lloyd D.M., Martyn I.D., Mashreghy-Mohammadi M.,
RA Matthews L., Mccann O.T., Mccloy J., McLaren S., Mcmurray A.A.,
RA Milne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V.,
RA Pearson S.D., Phillimore B.J., Phillips S.H., Plumb R.W., Ramsay H.,
RA Ramsey Y., Rogers L., Ross M.T., Scott C.E., Sehra H.K., Skuce C.D.,
RA Smalley S., Smith M.L., Soderlund C., Spragon L., Steward C.A.,
RA Stultson J.E., Swann R.M., Vaudin M., Wall M., Wallis J.M.,
RA Whiteley M.N., Willey D., Williams L., Williams S., Williamson H.,
RA Wilmer T.E., Wilming L., Wright C.L., Hubbard T., Bentley D.R.,
RA Beck S., Rogers J., Shimizu N., Minoshima S., Kawasaki K., Sasaki T.,
RA Asakawa S., Kudoh J., Shintani A., Shibuya K., Yoshizaki Y., Aoki N.,
RA Mitsuyma S., Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S.,
RA Do A., Do T., Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S.,
RA Lai H., Lao H.I., Lewis J., Lewis S., Lin S.-P., Lon P., Malat E.,
RA Nguyen T., Phan H., Phan S., Qi S., Qian Y., Ray L., Ren Q., Sheull S.,
RA Sloan D., Song L., Wang Q., Wang Y., Wang Z., White Y., Willingham D.,
RA Wu H., Yao Z., Zhan M., Zhang G., Chisoe S., Murray J., Miller N.,
RA Mix P., Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H.,
RA Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T.,
RA Haskins J., Hinds K., Kemp K., Latrelle P., Layman D., Ozesky P.,
RA Kollhoff T., Scheet P., Walker C., Wamsley A., Woldmann P., Pepin K.,
RA Nelson J., Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Budarf M.L., Mcdermott H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya H., Slamon M.I., Dunanski J.P.,
RA Peyrard K.P., Kedra D., Seroussi E., Franconi I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tilihan Y., Wright H.,
RA "The DNA sequence of human chromosome 22." ;
RA Nature 402:489-495(1999).
[3]
RP 3D-STRUCTURE MODELING OF 31-230.
RX MEDLINE=95111955; PubMed=7529123;
RX Bamford R.P., Hedgecock C.J., Richards W.G.;
RX "The Interleukin-2 and Interleukin-4 receptors studied by molecular
RX modeling." ;
RL structure 2:839-851(1994).
RT -
RT FUNCTION: RECEPTOR FOR INTERLEUKIN-2. THIS BETA SUBUNIT IS
RL INVOLVED IN RECEPTOR MEDIATED APOPTOSIS AND TRANSDUCES THE
CC MITOGENIC SIGNALS OF IL-2
CC -
CC SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
CC EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
CC AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CC CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
CC WITH A GAMMA CHAIN.
CC -
CC SUBCELLULAR LOCATION: Type I membrane protein.
CC -
CC SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -
CC DATABASE: NAME=PROW; NOTE=CD guide CD122 entry;
CC -
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd122.htm".
CC -
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -
DR EMBL; M25062; AAA59143.1; -
DR EMBL; AL022314; CNA18444.1; -
DR PIR; A50342; A50342.
DR PDB; 1ILM; 26-JAN-95.
DR PDB; 1ILN; 26-JAN-95.
DR MIM; 146710; -
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR003531; Hematopo_receptor_S.F1.
DR SMART; SM00060; FN3.1.
DR PROSITE; PS01355; HEMATOPO_REC_S.F1; 1.
KW Receptor; Transmembrane; Glycoprotein; signal; 3D-structure.

[illegible]


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QY 61 TCHMDVFEHMADDFSVNITDQSGNYSOBGCSFLAESIKRAPPENVTYTFSGOYNISMR 120
DB 80 TCHMDVFEHMADDFSVNITDQSGNYSOBGCSFLAESIKRAPPENVTYTFSGOYNISMR 139
QY 121 SDYEDPAFYMLKGLQYELQYRNKGDPMVSPRRKLISVDSRSVSLPLPERKDSYELQ 180
DB 140 SDYEDPAFYMLKGLQYELQYRNKGDPMVSPRRKLISVDSRSVSLPLPERKDSYELQ 199
QY 181 VRAGPMPGSSYOGTWSWSDPVIFOTQOSEELKEGMNPH 218
DB 200 VRAGPMPGSSYOGTWSWSDPVIFOTQOSEELKEGMNPH 237

RESULT 2
US-09-522-217-115
; Sequence 115, Application US/09522217
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; EARLIER FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-522-217-115

Query Match 100.0%; Score 1195; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 7.1e-123;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CPDLVCYTDYLOTVICILMMNLHPSTLTLTWODQYELKDEATSCSLHRSANHTATY 60
DB 20 CPDLVCYTDYLOTVICILMMNLHPSTLTLTWODQYELKDEATSCSLHRSANHTATY 79
QY 61 TCHMDVFEHMADDFSVNITDQSGNYSOBGCSFLAESIKRAPPENVTYTFSGOYNISMR 120
DB 80 TCHMDVFEHMADDFSVNITDQSGNYSOBGCSFLAESIKRAPPENVTYTFSGOYNISMR 139
QY 121 SDYEDPAFYMLKGLQYELQYRNKGDPMVSPRRKLISVDSRSVSLPLPERKDSYELQ 180
DB 140 SDYEDPAFYMLKGLQYELQYRNKGDPMVSPRRKLISVDSRSVSLPLPERKDSYELQ 199
QY 181 VRAGPMPGSSYOGTWSWSDPVIFOTQOSEELKEGMNPH 218
DB 200 VRAGPMPGSSYOGTWSWSDPVIFOTQOSEELKEGMNPH 237

RESULT 3
US-09-522-217-97
; Sequence 97, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
```

```
APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; EARLIER FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 97
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-zalalpha1 soluble receptor polypeptide sequence
US-09-522-217-97
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Query Match 100.0%; Score 1195; DB 4; Length 606;
Best Local Similarity 100.0%; Pred. No. 8.5e-123;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CPDLVCYTDYLOTVICILMMNLHPSTLTLTWODQYELKDEATSCSLHRSANHTATY 60
DB 389 CPDLVCYTDYLOTVICILMMNLHPSTLTLTWODQYELKDEATSCSLHRSANHTATY 448
QY 61 TCHMDVFEHMADDFSVNITDQSGNYSOBGCSFLAESIKRAPPENVTYTFSGOYNISMR 120
DB 449 TCHMDVFEHMADDFSVNITDQSGNYSOBGCSFLAESIKRAPPENVTYTFSGOYNISMR 508
QY 121 SDYEDPAFYMLKGLQYELQYRNKGDPMVSPRRKLISVDSRSVSLPLPERKDSYELQ 180
DB 509 SDYEDPAFYMLKGLQYELQYRNKGDPMVSPRRKLISVDSRSVSLPLPERKDSYELQ 568
QY 181 VRAGPMPGSSYOGTWSWSDPVIFOTQOSEELKEGMNPH 218
DB 569 VRAGPMPGSSYOGTWSWSDPVIFOTQOSEELKEGMNPH 606

RESULT 4
US-08-599-455B-2
; Sequence 2, Application US/08599455B
; Patent No. 5972621
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; APPLICANT: Culpepper, Janice A.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
; TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:41:41 ; Search time 43.94 Seconds

(without alignments)
90.053 Million cell updates/sec

Title: US-09-825-561A-10

Perfect score: 850
Sequence: 1 MRSSPGNMRIYICLMTYFL.....LLOKMIHQLSRTHGSEDS 162

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	850	100.0	162	4	US-09-522-217-2
2	695.5	81.8	519	4	US-09-522-217-85
3	486	57.2	146	4	US-09-522-217-56
4	394	46.4	510	4	US-09-522-217-89
5	212	24.9	40	4	US-09-522-217-72
6	176	20.7	32	4	US-09-522-217-73
7	99.5	11.7	114	1	US-08-031-399-6
8	99.5	11.7	114	1	US-08-031-398-12
9	99.5	11.7	114	1	US-08-393-305-3
10	99.5	11.7	114	1	US-08-726-817-3
11	99.5	11.7	114	1	US-08-504-042-6
12	99.5	11.7	114	1	US-08-504-042-12
13	99.5	11.7	114	2	US-08-725-969-3
14	99.5	11.7	114	2	US-08-794-524-3
15	99.5	11.7	114	4	US-09-189-193-3
16	99.5	11.7	114	5	PCT-US94-03793-6
17	99.5	11.7	114	5	PCT-US94-03793-12
18	99.5	11.7	162	1	US-08-031-399-5
19	99.5	11.7	162	1	US-08-393-305-2
20	99.5	11.7	162	1	US-08-535-733-2
21	99.5	11.7	162	1	US-08-726-817-2
22	99.5	11.7	162	1	US-08-504-042-5
23	99.5	11.7	162	1	US-08-725-969-2
24	99.5	11.7	162	2	US-08-794-524-2
25	99.5	11.7	162	3	US-08-842-947-6
26	99.5	11.7	162	4	US-09-189-193-2
27	99.5	11.7	162	4	US-09-522-217-113

28	99.5	11.7	162	5	PCT-US94-03793-5	Sequence 5, App1
29	99.5	11.7	162	5	PCT-US96-06423-2	Sequence 2, App1
30	94.5	11.1	114	1	US-08-031-399-3	Sequence 3, App1
31	94.5	11.1	114	1	US-08-393-305-6	Sequence 6, App1
32	94.5	11.1	114	1	US-08-726-817-6	Sequence 6, App1
33	94.5	11.1	114	1	US-08-504-042-3	Sequence 3, App1
34	94.5	11.1	114	2	US-08-725-969-6	Sequence 6, App1
35	94.5	11.1	114	2	US-08-794-524-6	Sequence 6, App1
36	94.5	11.1	114	4	US-09-189-193-6	Sequence 6, App1
37	94.5	11.1	114	5	PCT-US94-03793-3	Sequence 3, App1
38	94.5	11.1	122	1	US-08-300-903A-3	Sequence 3, App1
39	94.5	11.1	162	1	US-08-031-399-2	Sequence 2, App1
40	94.5	11.1	162	1	US-08-393-305-5	Sequence 5, App1
41	94.5	11.1	162	1	US-08-284-392B-9	Sequence 9, App1
42	94.5	11.1	162	1	US-08-726-817-5	Sequence 5, App1
43	94.5	11.1	162	1	US-08-504-042-2	Sequence 2, App1
44	94.5	11.1	162	2	US-08-725-969-5	Sequence 5, App1
45	94.5	11.1	162	2	US-08-794-524-5	Sequence 5, App1

ALIGNMENTS

RESULT 1
US-09-522-217-2
Sequence 2, Application US/09522217
Patent No. 6307024
GENERAL INFORMATION:
APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C. ?
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OR INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
EARLIER FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-09-522-217-2

Query Match 100.0%; Score 850; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 4.8e-87;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMRIYICLMTYFLGTLVHKSSGOGDRHMTBMQLDIYDQKNVNDLVPF 60
DB 1 MRSSPGNMRIYICLMTYFLGTLVHKSSGOGDRHMTBMQLDIYDQKNVNDLVPF 60
QY 61 LPAPDEVETNCWSAFCFOAKLSANTGNNEIIVNSIKLKRRPSTNAGROKRL 120
DB 61 LPAPDEVETNCWSAFCFOAKLSANTGNNEIIVNSIKLKRRPSTNAGROKRL 120
QY 121 TPCSDSYKKPKPELEFRKSLLOKMIHQLSRTHGSEDS 162
DB 121 TPCSDSYKKPKPELEFRKSLLOKMIHQLSRTHGSEDS 162

in particular T-lymphocyte-related disorders including atopic conditions such as asthma, allergy, rheumatoid arthritis, psoriasis, chronic inflammatory diseases and graft versus host disease, disorders involving the colon such as diarrhoea, dysentery, infectious enterocolitis, kidney disorders including polycystic kidney disease, cystic renal dysplasia, disorders of the thymus including lymphomas, Hodgkin disease and carcinoids. The 1645 polypeptides are also useful as modulating agents in cellular processes including growth promoting activity, particularly the antigen-independent proliferation of T-helper cell clones. The encoding nucleic acid is useful as primers or hybridization probes for the detection of IL-9/IL-2 receptor-like encoding nucleic acids and for tissue typing and in forensic biology. The present sequence represents the human IL-9/IL-2 receptor-like polypeptide (AAH16445).

Sequence 538 AA:

Query Match 100.0%; Score 1195; DB 22; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CPDLVCTDYDTLVTCILEMNLHPSTLTWQDYEELEKDEATSCSLHRAHNAHTATY 60
|||||
20 cpdlvctdydtlvtcilemnlhpsltltwqdyeelekeatscslhrahnahtaty 79
DB 61 TCHMDVHFHMADDFSVNITDQSGNYSQSGSFLLAESIKPAPPNVTVTFSGQYNISMR 120
|||||
80 tchmdvfhmaddifsvnitdsgnysqsgsfllaesikpappnvtvtfsgqynisw 139
DY 121 SDYEDPAFTMLKGLQYELQYRNKGDPMVAVSPRRKLISVDSRSVSLPLEFRKDSYELQ 180
|||||
DB 140 sdyedpafymlykglqyelqyrnrgdpmavsprrklisvdsrsvalplfrkdsyeld 199
DY 181 VRAGPMPGSSYOGTSEMSDPVIFOTOSPELKEGNPH 218
|||||
DB 200 vragpmpgssyogtsemsdpvifqtgeelkegnph 237

RESULT 9
AAH18629
ID AAB18629 standard; Protein: 606 AA.

AC AAB18629;
DT 22-JAN-2001 (first entry)
DE Amino acid sequence of MBP-human zalphall ligand fusion.
KW zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma; tumorigenesis; leukaemia; hematopoiesis; B cell tumour.

Synthetic.
OS Homo sapiens.

PN WO200053761-A2.

PD 14-SEP-2000.

PF 09-MAR-2000 / 2000WO-US06067.

PR 09-MAR-1999; 99US-0264908.
PR 11-MAR-1999; 99US-0265992.
PR 01-JUL-1999; 99US-0142013.

PA (ZYMO) ZYMOGENETICS INC.

PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA;
PI Johnston JV, Nelson AJ, Dillon SR, Hammond AK;

DR WPI: 2000-565600/52.
DR A-PSDB; AAA75609.

PT New human cytokine, designated zalphall ligand, useful for stimulating

the proliferation and/or development of haematopoietic cells in vitro and in vivo, and for treating tumourigenesis -

Example 45; Page 245-247; 256pp; English.

CC The present sequence represents a MBP-human zalphall ligand fusion.
CC zalphall ligand is a cytokine. The zalphall ligand is useful for
CC stimulating the proliferation and development of haematopoietic cells
CC in vitro and in vivo. zalphall ligand polynucleotides can be used as
CC primers or probes for cloning the zalphall gene. The zalphall ligand
CC is useful for treating tumourigenesis. A zalphall ligand-saporin fusion
CC toxin may be used for treating leukaemias and lymphomas. Antagonists
CC against zalphall ligand are useful as research reagents for
CC characterizing ligand-receptor interaction. Antagonists are also useful
CC for inhibiting expansion, proliferation, activation and differentiation
CC of cells involved in regulating hematopoiesis. The zalphall ligand may
CC also be used to stimulate an immune response against B cell tumour, a
CC virus, a parasite or a bacterium. The zalphall polypeptides,
CC polynucleotides, antagonists, agonists and antibodies are also useful
CC for the detection, diagnosis, prevention, and treatment of diseases
CC associated with a zalphall ligand genetic defect.

Sequence 606 AA:

Query Match 100.0%; Score 1195; DB 21; Length 606;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CPDLVCTDYDTLVTCILEMNLHPSTLTWQDYEELEKDEATSCSLHRAHNAHTATY 60
|||||
389 cpdlvctdydtlvtcilemnlhpsltltwqdyeelekeatscslhrahnahtaty 448
DB 61 TCHMDVHFHMADDFSVNITDQSGNYSQSGSFLLAESIKPAPPNVTVTFSGQYNISMR 120
|||||
449 tchmdvfhmaddifsvnitdsgnysqsgsfllaesikpappnvtvtfsgqynisw 508
DY 121 SDYEDPAFTMLKGLQYELQYRNKGDPMVAVSPRRKLISVDSRSVSLPLEFRKDSYELQ 180
|||||
DB 509 sdyedpafymlykglqyelqyrnrgdpmavsprrklisvdsrsvalplfrkdsyeld 568
DY 181 VRAGPMPGSSYOGTSEMSDPVIFOTOSPELKEGNPH 218
|||||
DB 569 vragpmpgssyogtsemsdpvifqtgeelkegnph 606

RESULT 10

AAH79316
ID AAH79316 standard; Protein: 606 AA.

AC AAH79316;

DT 18-JUL-2000 (first entry)

DE Maltose binding protein-zalphall fusion protein.

KW Cytokine receptor; zalphall; maltose binding protein; human;
KW apoptosis; signal transduction; growth factor; cancer; tumour;
KW infection; gene therapy; diagnosis; muzalphall/MBP-6H.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Protein 1..388 "maltose binding protein"

FT Protein 389..606 /note="zalphall cytokine binding domain"

PN WO200017235-A2.

PD 30-MAR-2000.

PT 23-SEP-1999; 99WO-US22149.

XX 23-SEP-1998; 98US-0159254.
 PR 09-MAR-1999; 99US-0265117.
 PR 06-JUL-1999; 99US-0347930.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 PI Presnell SR, Conklin DC, Novak JE, Hammond AR;
 DR WPI: 2000-292825/25.
 DR N-PSDB; AA294554.
 XX
 PT Novel nucleic acid encoding zalpahal polypeptide, useful for treating
 PT e.g. viral infection or tumors, and for identifying ligands that
 PT stimulate cell proliferation
 XX
 PS Example 13; Page 166-168; 190pp; English.

The present sequence is that of a fusion protein, designated huzalpalhal/MBP-6H, comprising a maltose binding protein (MBP) fused to the cytokine binding domain (amino acids 20-237) of human class I cytokine receptor zalpahal (see AA79312). An expression plasmid containing huzalpalhal/MBP-6H DNA (see AA294554) was constructed via homologous recombination and the fusion protein CC was expressed in Escherichia coli BL21 using vector plasmid pTAP98. CC cell signalling molecule, growth factor receptor, or is a CC extracellular matrix associated protein with growth factor hormone CC activity. The invention provides zalpahal polypeptides (including CC fusion proteins), polynucleotides and antibodies, and methods for CC their use in the treatment and diagnosis of conditions associated CC with altered zalpahal expression or activity.

XX Sequence 606 AA;

Query Match 100.0%; Score 1195; DB 21; Length 606;
 Best Local Similarity 100.0%; Pred. No. 1.9e-115;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCTDYLTQVYICILEMNLHPSTLTFTWQDYELKDEATSCSLHRSANHTATY 60
 Db 389 cpdlvctdylytqvtcllemwnlhpstltftwqdyeelkdeatcschlrsahnaty 448
 QY 61 TCHMDVFHMDADIFSVNTDQSGNYSGEGSFLLAESIKPAPFNVTWTPSGQYNISWR 120
 449 tchmdvfhmaddifsvntdsgnysgegsfllaesikpappfnvltwtpsgqyniswr 508
 QY 121 SDYEDPAFYMLKGLQYELQYRNKGDPMWAVSPRRKLISVDSRYSLLPLEFRKDSYELQ 180
 509 sdyedpatfymkglqyelqyrnrgdpmwavsprkrlisvdsrsvsllplefrkdsyelo 568
 QY 181 VRAGPMGSSYOGTSEMSDPVIFQTOSEELKEGMNPH 218
 Db 569 vragpmpgssyogtsemsdpvifqtoseelkegmnpn 606

RESULT 11

AA294304
 ID AA294304 standard; Protein: 538 AA.

AC AA294304;

DT 08-AUG-2000 (first entry)

DE Human HNOVILR polypeptide 1.

XX Human; anticancer; anti-inflammatory; immunosuppressive; anti-allergic;
 KM antiasthmatic; antirheumatic; antiarthritic; nootropic; vasotropic;
 KM neuroprotective; antibacterial; cerebroprotective; osteopathic;
 KM hepatoprotective; hypotensive; hypertensive; antifungal;
 KM anti-HIV; antiprotocoll; antiviral; antianemic; autoimmune disease;
 KM Crohn's disease; Alzheimer's disease; Parkinson's disease; stroke;

KM multiple sclerosis; cancer; infection; cardiovascular disease.
 XX Homo sapiens.
 OS
 XX WO200027882-A1.
 PN
 XX 18-MAY-2000.
 PD
 XX 01-NOV-1999; 99WO-US25617.
 PF
 XX 06-NOV-1998; 98US-0187711.
 PR
 XX (SMK) SMITHKLINE BEECHAM CORP.
 PA
 PI Kikly NK, Michalovich D;
 DR WPI: 2000-376497/32.
 DR N-PSDB; AA26984.

PT Isolated polypeptide of HNOVILR type used for diagnosing or treating
 PT for example cancer, inflammation, autoimmune disease -
 XX
 PS Claim 1; Page 30-31; 36pp; English.

The present sequence is a HNOVILR polypeptide which is believed to be a member of the cytokine receptor family of polypeptides. It shows CC homology with human interleukin receptor 2 and is therefore expected CC to have similar biological functions/properties. The polynucleotide may be CC obtained from a cDNA library derived from mRNA in cells of human bone CC marrow using expressed sequence tag (EST) analysis. Alternatively it CC can be synthesised using commercially available techniques. The growth, CC regulation and functional activities of cells are regulated through the CC interaction of cytokines and their cognate receptors. Thus the CC gene sequence and its product are useful for diagnosing or treating a CC wide range of diseases including cancer, inflammation, autoimmune CC disease, Crohn's disease, allergy, asthma, rheumatoid arthritis, CC Alzheimer's disease, Parkinson's disease, multiple sclerosis, CC head injury damage, septic shock, stroke, osteoporosis, osteoarthritis, CC cardiovascular disease, kidney disease, liver disease, ischemic injury, CC myocardial infarction, hypotension, hypertension, acquired immune CC deficiency syndrome (AIDS), male pattern baldness, and bacterial, CC fungal, protozoan and viral infections.

SO Sequence 538 AA;

Query Match 99.4%; Score 1188; DB 21; Length 538;
 Best Local Similarity 99.5%; Pred. No. 8.5e-115;
 Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPDLVCTDYLTQVYICILEMNLHPSTLTFTWQDYELKDEATSCSLHRSANHTATY 60
 Db 20 cpdlvctdylytqvtcllemwnlhpstltftwqdyeelkdeatcschlrsahnaty 79
 QY 61 TCHMDVFHMDADIFSVNTDQSGNYSGEGSFLLAESIKPAPFNVTWTPSGQYNISWR 120
 Db 80 tchmdvfhmaddifsvntdsgnysgegsfllaesikpappfnvltwtpsgqyniswr 139
 QY 121 SDYEDPAFYMLKGLQYELQYRNKGDPMWAVSPRRKLISVDSRYSLLPLEFRKDSYELQ 180
 Db 140 sdyedpatfymkglqyelqyrnrgdpmwavsprkrlisvdsrsvsllplefrkdsyelo 199
 QY 181 VRAGPMGSSYOGTSEMSDPVIFQTOSEELKEGMNPH 218
 Db 200 vragpmpgssyogtsemsdpvifqtoseelkegmnpn 237

RESULT 12

AA008728
 ID AA008728 standard; Protein: 538 AA.

AC AA008728;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:44:30 ; Search time 63.41 Seconds

(without alignments)
594.747 Million cell updates/sec

Title: US-09-825-561A-6

Perfect score: 1195
Sequence: 1 CPVLVCYTPYLTIVICILEM.....SDPVIFQTSSEELKSGMNP 218

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

arched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_plant:*
- 10: sp_rodent:*
- 11: sp_virus:*
- 12: sp_vertebrate:*
- 13: sp_unclassified:*
- 14: sp_virus:*
- 15: sp_bacteriap:*
- 16: sp_archaeap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1195	100.0	538	4 Q9HBE5	Q9HBE5 homo sapien
2	1195	100.0	538	4 Q9HBE1	Q9HBE1 homo sapien
3	844	70.6	529	11 Q9JHX3	Q9JHX3 mus muscula
4	838	70.1	529	11 Q9ESM1	Q9ESM1 mus muscula
5	162.5	13.6	896	11 Q64146	Q64146 rattus norv
6	155.5	13.0	890	11 Q921A0	Q921A0 cavia porce
7	144	12.1	1162	11 Q9QMG3	Q9QMG3 mus musculu
8	138	11.5	895	11 Q62960	Q62960 rattus norv
9	137	11.5	896	4 Q92919	Q92919 homo sapien
10	137	11.5	958	4 Q92920	Q92920 homo sapien
11	137	11.5	1165	4 Q92921	Q92921 homo sapien
12	136	11.4	896	4 Q13594	Q13594 homo sapien
13	136	11.4	906	4 Q13593	Q13593 homo sapien
14	136	11.4	958	4 Q13592	Q13592 homo sapien
15	135.5	11.3	825	4 Q96P01	Q96P01 homo sapien
16	135	11.3	894	6 Q9MYL1	Q9MYL1 macaca mula

17	135	11.3	925	6 Q9MYK9	Q9MYK9 macaca mula
18	135	11.3	1163	6 Q9MYL2	Q9MYL2 macaca mula
19	135	11.3	1194	6 Q9MYL0	Q9MYL0 macaca mula
20	134	11.2	1148	13 Q91BA7	Q91BA7 gallus gall
21	132.5	11.1	566	11 Q925F5	Q925F5 sus scrofa
22	132	11.0	848	6 Q9MZS2	Q9MZS2 sus scrofa
23	129	10.8	1165	6 Q02671	Q02671 sus scrofa
24	127.5	10.7	861	6 Q9HBG2	Q9HBG2 bos taurus
25	125	10.5	1147	13 Q9DDK1	Q9DDK1 meleagris g
26	124.5	10.4	1146	13 Q91BY6	Q91BY6 gallus gall
27	123	10.3	459	4 Q90PC1	Q90PC1 homo sapien
28	120	10.0	234	6 Q97888	Q97888 bos taurus
29	117	9.8	810	11 Q54690	Q54690 mus musculu
30	117	9.8	801	11 Q60583	Q60583 mus musculu
31	116	9.7	881	13 Q57519	Q57519 xenopus lae
32	115.5	9.7	229	11 Q9RIW8	Q9RIW8 rattus norv
33	115	9.6	459	11 Q9ROCI	Q9ROCI mus musculu
34	114.5	9.6	343	13 Q9DEQ1	Q9DEQ1 oncorhynch
35	114.5	9.6	801	11 Q9WTM8	Q9WTM8 rattus norv
36	113.5	9.5	800	11 Q63257	Q63257 rattus norv
37	112.5	9.4	422	4 Q75462	Q75462 homo sapien
38	111.5	9.3	422	4 Q9UHS5	Q9UHS5 homo sapien
39	111.5	9.3	425	11 Q9JMS8	Q9JMS8 mus musculu
40	108.5	9.1	415	11 Q920K4	Q920K4 cavia porce
41	106	8.9	638	6 Q9TU69	Q9TU69 canis faml
42	105.5	8.8	628	11 Q9JRG1	Q9JRG1 cavia porce
43	105	8.8	521	4 Q96TF0	Q96TF0 homo sapien
44	101.5	8.5	509	6 Q9MYZ9	Q9MYZ9 sus scrofa
45	101	8.5	386	6 Q951F0	Q951F0 canis faml

ALIGNMENTS

RESULT 1

Q9HBE5 PRELIMINARY; PRT; 538 AA.

AC Q9HBE5;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE INTERLEUKIN 21 RECEPTOR.

GN IL21R.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID:9606;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=11081504;

RA Parish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C., Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S., Burkhead S., Helpe M., Brandt C., Kuljper J., Kramer J., Conklin D., Presnell S.R., Berry J., Shiota F., Bort S., Handily K., Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T., Raymond F., Ra Ching A., Yao L., Smith D., Webster P., Whitmore T., Maurer M., Kushnarsky K., Holly R.D., Foster D., "Interleukin 21 and its receptor are involved in NK cell expansion and regulation of lymphocyte function.", Nature 408:57-63(2000).

RT Nature 408:57-63(2000).

RL [2]

RP SEQUENCE FROM N.A.

RP TISSUE=LYMPHOMA;

RA Strausberg R.; Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF254067; AAC29346.1; -

DR EMBL: BC004348; AAH04348.1; -

DR InterPro: IPR003961; FN_III.

DR SMART: SMD0060; FN3; 1.

KW Receptor.

SQ SEQUENCE 538 AA; 59129 MW; 414079CCB974850A CRC64;

Query Match 100.0%; Score 1195; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.2e-110;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCTDYLVQVVICILEMNNLHPSTLTLTWODOYEELKDEATSCSLHRSANATHARY 60
DB 20 CPDLVCTDYLVQVVICILEMNNLHPSTLTLTWODOYEELKDEATSCSLHRSANATHARY 79
QY 61 TCHMDVHFHMADDFSVNITDQSGNSQECGFLAESIKPAPFNVTVTFSGQYINISMR 120
DB 80 TCHMDVHFHMADDFSVNITDQSGNSQECGFLAESIKPAPFNVTVTFSGQYINISMR 139
QY 121 SDVEDPAFYMLKGLQYELQYRNRRGDPMAVSPRRKLISVDSRSVSLPLEFRKDSSEYLO 180
DB 140 SDVEDPAFYMLKGLQYELQYRNRRGDPMAVSPRRKLISVDSRSVSLPLEFRKDSSEYLO 199
QY 181 VRAGPMGSSYOGTWSWSDPVIFOTQSEELKEGNMNP 218
DB 200 VRAGPMGSSYOGTWSWSDPVIFOTQSEELKEGNMNP 237

SULT 2
ID 09HB91 PRELIMINARY; PRT: 538 AA.
AC 09HB91;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE NOVEL INTERLEUKIN RECEPTOR.
GN NILR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20481926; PubMed=11016959;
RA Ozaki K., Kikly K., Michalovich D., Young P.R., Leonard W.J.;
RT "Cloning of a type I cytokine receptor most related to the IL-2
RT receptor beta chain."
RL Proc. Natl. Acad. Sci. U.S.A. 97:11439-11444(2000).
DR EMBL: AF269133; AAC23419.1; -
DR InterPro: IPR003961; FN.LII.
DR SMART: SM00060; FN3; I.
KW Receptor.
SQ SEQUENCE 538 AA; 59228 MW; 23D7F3EDFC74915B CRC64;

Query Match 70.6%; Score 844; DB 11; Length 529;
Best Local Similarity 69.3%; Pred. No. 1.1e-75;
Matches 151; Conservative 31; Mismatches 36; Indels 0; Gaps 0;

QY 1 CPDLVCTDYLVQVVICILEMNNLHPSTLTLTWODOYEELKDEATSCSLHRSANATHARY 60
DB 20 CLDLCTCTDYLVQVVICILEMNNLHPSTLTLTWODOYEELKDEATSCSLHRSANATHARY 79
QY 61 TCHMDVHFHMADDFSVNITDQSGNSQECGFLAESIKPAPFNVTVTFSGQYINISMR 120
DB 80 TCHMDVHFHMADDFSVNITDQSGNSQECGFLAESIKPAPFNVTVTFSGQYINISMR 139
QY 121 SDVEDPAFYMLKGLQYELQYRNRRGDPMAVSPRRKLISVDSRSVSLPLEFRKDSSEYLO 180
DB 140 SDVEDPAFYMLKGLQYELQYRNRRGDPMAVSPRRKLISVDSRSVSLPLEFRKDSSEYLO 199
QY 181 VRAGPMGSSYOGTWSWSDPVIFOTQSEELKEGNMNP 218
DB 200 VRAGPMGSSYOGTWSWSDPVIFOTQSEELKEGNMNP 237

RESULT 4
ID 09ESM1 PRELIMINARY; PRT: 529 AA.
AC 09ESM1;
DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE NOVEL CYTOKINE RECEPTOR NR8.
 GN IL2IR OR NR8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RA Nomura H., Yaguchi N., Maeda M., Hasegawa M.;
 RT "A novel cytokine receptor NR8 is closely mapped to IL-4R:
 RT Polymorphism in Balb/c mouse.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB045137; BAB13736.1; -.
 DR MGD; MGI:1890475; 1121r.
 DR InterPro; IPR003961; FN_III.
 DR SMART; SM00060; FN3; 1.
 SO RECEPTOR.
 50 SEQUENCE 529 AA; 58358 MW; 212834822AA7722B CRC64;

Query Match 70.1%; Score 838; DB 11; Length 529;
 Best Local Similarity 68.3%; Pred. No. 4.5e-75;
 Matches 149; Conservative 33; Mismatches 36; Indels 0; Gaps 0;

QY 1 CPDLYTDTYLTQVTCILEMNLHPSTLTLLTWQDYELKDEATSCSLHRSANHTATY 60
 DB 20 CIDLTYTTLTWTTCVLTETRSNPSTLSLTWQDEYELQDDETCSLHRSCHNTHTMY 79
 QY 61 TCHMDVFHMAADDIFSVNTIDSGNYSQEGSFLAESIKPAPNNVTFSGQYINSMR 120
 DB 80 TCHMRISQFLSDSEVFTVNTIDSGNNSQEGSFLAESIKPAPNNVTFSGRDISMD 139
 QY 121 SYEDPAFYMLKGLQYELQYRNKGDPMVSPRRKLISVDSKSVSLPLEERKDSYELQ 180
 DB 140 SADEPSNVLRLKQLQYELQYRNLRNPVAPVPTKLISVDSKSVSLPLEERKDSYELQ 199
 QY 181 VRAPMGSSYOGTSEMSDPIYFOTQSELEKEGNPH 218
 DB 200 MRAAPQGTSPFRTGSEMSDPIYFOTQGEPLAGWDPH 237

RESULT 5
 064146 PRELIMINARY; PRT; 896 AA.

064146:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DE 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).
 GN IL-3R<BETA>.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95370942; PubMed=7643220;
 RA Appel K., Butlini M., Sauter A., Gebicke-Haerter P.J.;
 RT "Cloning of rat interleukin-3 receptor beta-subunit from cultured
 RT microglia and its mRNA expression in vivo.";
 RL J. Neurosci. 15:5800-5809(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MISTAR; TISSUE=BRAIN;
 RA Gebicke-Haerter P.J.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; S79263; AAB35068.1; -.
 DR EMBL; AJ000555; CAA04186.1; -.
 DR InterPro; IPR002996; CRIA.
 DR InterPro; IPR000282; Cytok_receptor_2.

DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003531; Hematopo_receptor_S_FL.
 DR Pfam; PFC00041; fn3; 2.
 DR SMART; SM00060; FN3; 2.
 DR PROSITE; PS01355; HEMATOPO_REC_S_FL; UNKNOWN_1.
 KW Signal.
 FT NON_TER 1 1
 FT NON_TER 896 896
 SO SEQUENCE 896 AA; 99504 MW; 4C6E3B288A4A1052 CRC64;

Query Match 13.6%; Score 162.5; DB 11; Length 896;
 Best Local Similarity 25.1%; Pred. No. 1.7e-07;
 Matches 59; Conservative 32; Mismatches 89; Indels 55; Gaps 9;

QY 4 LVCYTDYLTQVTCILEMNLHPSTLTLLTWQDYELKDEATSCSL----- 48
 DB 37 LQCYNDYIERILCSWADTEDAQLVNLTLTYHWD-----VKQAHVQPPPP 91
 QY 49 HRSANHTATYT-----CHMDVFHMAADDIFSVNTIDSGNYSQEGSFLAESIKPAP 104
 DB 92 HRCVPRRCVLPYTFQSVSKEDYTSLOPDRDLSTHLV-----VPLAQHVQPPPP 139
 QY 105 FNYTFESG-QYINISWRSYEDPAFYMLKGLQYELQYRNKGDPMVSPRRKLISVDSR 162
 DB 140 KDLSISPSGDHFLKMSVPLGDAQVSLLSQKDQFVAVKQIQDSWE-----DAS 189
 QY 163 S-----VSLPLEERKDSYELQYRAGPMGSSYOGTSEMSDPIYFOTQSEE 210
 DB 190 SLHTCMVLTLEKPLPLPNSIYAVRAQLAPGSSLSGRPSGMSPEVHMDSTED 244

RESULT 6
 0921A0 PRELIMINARY; PRT; 890 AA.

AC 0921A0:
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE INTERLEUKIN-5 RECEPTOR BETA CHAIN.
 GN IL5.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Logsdon N.J., Graham A., Scott C.W.;
 RT "Guinea pig IL5 receptor beta chain.";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U94688; AAC77520.1; -.
 DR HSSP; P40189; 1BQV.
 DR InterPro; IPR002996; CRIA.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003531; Hematopo_receptor_S_FL.
 DR Pfam; PF00041; fn3; 3.
 DR SMART; SM00060; FN3; 2.
 DR PROSITE; PS01355; HEMATOPO_REC_S_FL; UNKNOWN_1.
 KW Receptor.
 SO SEQUENCE 890 AA; 96579 MW; D43FB1CA8852536 CRC64;

Query Match 13.0%; Score 155.5; DB 11; Length 890;
 Best Local Similarity 26.5%; Pred. No. 8.6e-07;
 Matches 57; Conservative 33; Mismatches 78; Indels 47; Gaps 10;

QY 3 DLVCYTDYLTQVTCILEMNLHPSTLTLLTWQDYELKDEATSCSL----- 46
 DB 250 NLQGVFPGATILCSMWVRVSQVTSVSGFLFYRSSLDAGEQCPQYQKELHDITRRSC 309
 QY 47 SLHRSANHTATYTCHMDVFHMAADDIFSVNTIDSGNYSQEGSFLAESIKPAP 105
 DB 310 QI-RVSNRPHSQYT-----VTVPRNGEKFLRSANHTQMA-----APTL 348

QY 106 NATVFSGQYINISMSRSDYEDPAFYMLKGLQYELQYRNKGDPAVSPRRKLISYDSRSVS 165
 DB 349 NATKID-GDYSLKAWTE---KMYSHIENTFEIQYRAGDWMENSKETEL--KNAHMP 401
 QY 166 LPLFRKDSYELQYRAGPMGSSYQGTWSEMSD 200
 DB 402 LPPLE--PATTYLAIRVAKPFGAGYNGIMSEMS 434

RESULT 7
 Q90WG3 PRELIMINARY; PRT; 1162 AA.
 AC Q90WG3;
 DT 01-MAY-2000 (Tremblrel, 13, Created)
 DT 01-MAY-2000 (Tremblrel, 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)
 DE LEPTIN RECEPTOR B.
 GN LEPR OR LEPRB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KK OBES; TISSUE=BRAIN, HYPOTHALAMUS;
 RA Igel M., Taylor B.A., Phillips S.J., Becker W., Herberg L.,
 RA Joost H.G.;
 RT "Hypoleptinemia and leptin receptor variant Asp600Asn in the obese,
 RT hyperinsulinemic KK mouse strain."
 RL J. Endocrinol. 21:337-345 (1998).
 DR EMBL; Y10296; CA471342.1; -.
 DR HSSP; P16471; 1BP3.
 DR MGD; MG1:104993; Lepr.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam; PF00041; fn3; 3.
 DR SMART; SM00060; FN3; 3.
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 KW Receptor.
 FT VARIANT 600 600 N -> D.
 SQ SEQUENCE 1162 AA; 130787 MW; 541E77CBB46EC00D CRC64;

Query Match 12.1%; Score 144; DB 11; Length 1162;
 Best Local Similarity 31.1%; Pred. No. 1.7e-05;
 Matches 57; Conservative 22; Mismatches 60; Indels 44; Gaps 11;

DB 39 LKDE---ATSCLSHSAHNAHTATYCHMDVFH-----FMADDIFSVNITDQSGNYS 87
 DB 177 LKDSFQTVQNCISLRGC-----ECHVPVPRAKNLVALLMYLETISAGVSFQSPILMS 227
 QY 88 QECGSEFLASIKPAP--FNVTVFSGQYINISMSRSDYEDPAFYMLKGLQYELQYRNNG 145
 DB 228 LQ--PMV---VKPDPPLGLRMEVTDGINKISWDSQTKAPF-----PLOYQVYLEMS 276
 QY 146 DPMVAVSPRRKLISYDSRSV-SLPLFRKDSYELQYRAGPMGSSYQGTWSEMSDPIYF 204
 DB 277 T--IVREAIEIVSDSLVDVLP-----GSSYEQVRSKRILDS---GVWSDMSPOVF 326
 QY 205 QTO 207
 DB 327 TTD 329

RESULT 8
 Q62960 PRELIMINARY; PRT; 895 AA.
 AC Q62960;
 DT 01-NOV-1996 (Tremblrel, 01, Created)

DT 01-NOV-1996 (Tremblrel, 01, Last sequence update)
 DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)
 GN LEPTIN RECEPTOR.
 DE ROB-R.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
 RA Wang M.-Y., Unger R.H.;
 RT "Characterization of leptin receptors in normal and Zucker diabetic
 RT fatty rats."
 RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL; U53144; AAB03088.1; -.
 DR HSSP; P16471; 1BP3.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam; PF00041; fn3; 2.
 DR SMART; SM00060; FN3; 1.
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 895 AA; 101324 MW; 3C93F018A737C07 CRC64;

Query Match 11.5%; Score 138; DB 11; Length 895;
 Best Local Similarity 30.9%; Pred. No. 4.8e-05;
 Matches 56; Conservative 23; Mismatches 62; Indels 40; Gaps 11;

QY 39 LKD--EATSCLSHSAHNAHTATYCHMDVFH-----FMADDIFSVNITDQSGNYSQ 89
 DB 177 LKDSFQTVQNCISLRGC-----NCSVRECECHVPVPRAKNVYALLMYLETISAGVSFQSPILMS 229
 QY 90 CGSEFLAESIKPAP--FNVTVFSGQYINISMSRSDYEDPAFYMLKGLQYELQYRNBDP 147
 DB 230 --PMV---VKPDPPLGLRMEVTDGINKISWDSQTKAPF-----PLOYQVYLENST- 277
 QY 148 WAVSPRRKLISYDSRSV-SLPLFRKDSYELQYRAGPMGSSYQGTWSEMSDPIYFOT 206
 DB 278 -IVREAIEIVSDSLVDVLP-----GSSYEQVRSKRILDS---GVWSDMSLQLFTT 328
 QY 207 Q 207
 DB 329 Q 329

RESULT 9
 Q92919 PRELIMINARY; PRT; 896 AA.
 AC Q92919;
 DT 01-FEB-1997 (Tremblrel, 02, Created)
 DT 01-FEB-1997 (Tremblrel, 02, Last sequence update)
 DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)
 DE LEPTIN RECEPTOR.
 GN DB.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,
 RA Matthews W.,
 RL Curr. Biol. 6:0-0(0).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97215244; PubMed=9061609;
 RA Luch S.M., Di Marco F., Levin N., Armanini M., Xie M.H., Nelson C.,
 RA Bennett G.L., Williams M., Spencer S.A., Gurney A., de Sauvage F.J.;

RT "Cloning and characterization of a human leptin receptor using a
RT biologically active leptin immunoadhesin."
RL J. Mol. Endocrinol. 18:77-85(1997).
DR EMBL; U66495; AAB07495.1; -
DR EMBL; U50748; AAC23650.1; -
DR HSSP; P16471; 1BP3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
SQ SEQUENCE 896 AA; 102489 MW; D371C7A186DEE3 CRC64;

Query Match 11.5%; Score 137; DB 4; Length 896;
Best Local Similarity 28.0%; Pred. No. 6e-05;
Matches 47; Conservative 25; Mismatches 68; Indels 28; Gaps 8;

QY 45 SCSLHSAHNAHTATYTCMDVHFHMAD--IFSVNITDQSGNYSQEGSFLAESIKPA 102
DB 187 NCSVHECC-----CLVPVPTAKLNDTLMLCKITSGVIFQSPPLMSYQPINMKPD 238
QY 103 PP--FNVTYTFSGOYNISMRSDYEDPAFYMLKGLQYELQYRNRRGDPMAVSRRKLISVD 160
DB 239 PPLGLHMEITDDGNLKISWSSP-----PLVPFPIQYQKY-SENSTYIVREADKIVSAT 291
QY 161 SRSV-SLLPLEFRKDSYELQYRAGMPGSSYQGTWSEMSDPYIRQTQ 207
DB 292 SLIVDSILP-----GSSYEVOYGRKRLDG---PGIMSDWSTPRVPTTQ 331

RESULT 10
Q92920 PRELIMINARY; PRT; 958 AA.
AC Q92920;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LEPTIN RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid-9606;
N [1]
P SEQUENCE FROM N.A.
RA MEDLINE-96398968; PubMed-8805376;
RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,
RA Mathews W.;
RT "A role for leptin and its cognate receptor in hematopoiesis."
RL Curr. Biol. 6:1170-1180(1996).
DR EMBL; U66496; AAB07496.1; -
DR HSSP; P16471; 1BP3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 958 AA; 109392 MW; 3F5BC5A187E803A CRC64;

Query Match 11.5%; Score 137; DB 4; Length 958;
Best Local Similarity 28.0%; Pred. No. 6.6e-05;
Matches 47; Conservative 25; Mismatches 68; Indels 28; Gaps 8;
QY 45 SCSLHSAHNAHTATYTCMDVHFHMAD--IFSVNITDQSGNYSQEGSFLAESIKPA 102
DB 187 NCSVHECC-----CLVPVPTAKLNDTLMLCKITSGVIFQSPPLMSYQPINMKPD 238

DB 187 NCSVHECC-----CLVPVPTAKLNDTLMLCKITSGVIFQSPPLMSYQPINMKPD 238
QY 103 PP--FNVTYTFSGOYNISMRSDYEDPAFYMLKGLQYELQYRNRRGDPMAVSRRKLISVD 160
DB 239 PPLGLHMEITDDGNLKISWSSP-----PLVPFPIQYQKY-SENSTYIVREADKIVSAT 291
QY 161 SRSV-SLLPLEFRKDSYELQYRAGMPGSSYQGTWSEMSDPYIRQTQ 207
DB 292 SLIVDSILP-----GSSYEVOYGRKRLDG---PGIMSDWSTPRVPTTQ 331

RESULT 11
Q92921 PRELIMINARY; PRT; 1165 AA.
AC Q92921;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LEPTIN RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid-9606;
N [1]
P SEQUENCE FROM N.A.
RA MEDLINE-96398968; PubMed-8805376;
RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,
RA Mathews W.;
RT "A role for leptin and its cognate receptor in hematopoiesis."
RL Curr. Biol. 6:1170-1180(1996).
DR EMBL; U66497; AAB07497.1; -
DR HSSP; P16471; 1BP3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hematopo_receptor_L_F2.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 1165 AA; 132493 MW; CAA03BEAF2602D0A CRC64;

Query Match 11.5%; Score 137; DB 4; Length 1165;
Best Local Similarity 28.0%; Pred. No. 8.4e-05;
Matches 47; Conservative 25; Mismatches 68; Indels 28; Gaps 8;

QY 45 SCSLHSAHNAHTATYTCMDVHFHMAD--IFSVNITDQSGNYSQEGSFLAESIKPA 102
DB 187 NCSVHECC-----CLVPVPTAKLNDTLMLCKITSGVIFQSPPLMSYQPINMKPD 238
QY 103 PP--FNVTYTFSGOYNISMRSDYEDPAFYMLKGLQYELQYRNRRGDPMAVSRRKLISVD 160
DB 239 PPLGLHMEITDDGNLKISWSSP-----PLVPFPIQYQKY-SENSTYIVREADKIVSAT 291
QY 161 SRSV-SLLPLEFRKDSYELQYRAGMPGSSYQGTWSEMSDPYIRQTQ 207
DB 292 SLIVDSILP-----GSSYEVOYGRKRLDG---PGIMSDWSTPRVPTTQ 331

RESULT 12
Q13594 PRELIMINARY; PRT; 896 AA.
AC Q13594;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE B219/OB RECEPTOR ISOFORM HUB219.3 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid-9606;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:42:52 ; Search time 65.65 seconds
(without alignments)
319,078 Million cell updates/sec

Title: US-09-825-561a-6

Perfect score: 1195
Sequence: 1 CPDLVCYTDYLTQTVICILEM.....SDPVIFQTSSELEKGNPH 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pirl:1*
2: pirl:2*
3: pirl:3*
4: pirl:4*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162.5	13.6	878	1 I56563	interleukin-3 rece
2	145	12.1	896	2 A40091	interleukin-3 rece
3	144	12.1	805	2 S68441	leptin receptor, s
4	144	12.1	892	2 S68439	leptin receptor, s
5	144	12.1	894	2 S68437	leptin receptor, s
6	144	12.1	896	1 A35782	cytokine receptor
7	144	12.1	900	2 S68440	leptin receptor, s
8	144	12.1	1162	2 S68438	leptin receptor, s
9	141.5	11.8	539	2 A35052	interleukin-2 rece
10	139	11.6	579	2 B45266	MPL-K protein prec
11	139	11.6	635	2 A45266	MPL-K protein prec
12	138	11.5	895	2 S74225	leptin receptor, 1
13	138	11.5	1162	2 PC4184	leptin receptor, O
14	135.5	11.3	825	1 A60386	interleukin-4 rece
15	134	11.2	537	2 B46535	interleukin-2 rece
16	133.5	11.2	369	2 I49280	interleukin-2 rece
17	132.5	11.1	625	2 S35317	hematopoietic grow
18	132.5	11.1	626	2 S37622	proto-oncogene - m
19	127	10.6	373	2 A53718	interleukin-2 rece
20	126	10.5	551	2 A30342	interleukin-2 rece
21	123	10.3	262	2 C34791	interleukin-7 rece
22	123	10.3	298	2 B34791	interleukin-7 rece
23	123	10.3	459	2 A34791	interleukin-7 rece
24	122	10.2	831	2 J01655	prolactin receptor
25	121.5	10.2	918	2 A44257	interleukin-6 sign
26	120	10.0	369	2 A44255	interleukin-2 rece
27	117	9.9	897	1 A39255	cytokine receptor
28	117	9.8	810	1 A33380	interleukin-4 rece
29	115	9.6	459	2 D34791	interleukin-7 rece

30	113.5	9.5	284	2 S27931	Env/v-mpl fusion p
31	113.5	9.5	800	1 S31575	interleukin-4 rece
32	112.5	9.4	917	2 I49699	glycoprotein 130 -
33	110.5	9.2	918	2 A36337	membrane glycoprot
34	108.5	9.1	468	1 A41242	interleukin-6 rece
35	106	8.9	638	2 S12136	interleukin-6 rece
36	105.5	8.8	279	2 B32985	somatotropin recep
37	105.5	8.8	440	2 J10144	somatotropin-bindl
38	105.5	8.8	460	2 J10145	interleukin-6 rece
39	105.5	8.8	638	2 A33505	somatotropin recep
40	105	8.8	522	2 B45268	interleukin-9 rece
41	104	8.7	638	2 B28176	somatotropin recep
42	103	8.6	508	1 Z0H0R	erythropoietin rec
43	102	8.5	468	2 A45268	interleukin-9 rece
44	100.5	8.4	265	2 S14081	erythropoietin rec
45	99.5	8.3	507	1 A32385	erythropoietin rec

ALIGNMENTS

RESULT 1
I56563
interleukin-3 receptor beta-subunit - rat
C:Species: Rattus sp. (rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
C:Accession: I56563
R:Appel, K.; Butlini, M.; Sauter, A.; Gebicke-Haerter, P.J.
J. Neurosci. 15, 5800-5809, 1995
A:Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia a
A:Reference number: I56563; MUID:95370942
A:Accession: I56563
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-896 <RES>
A:Cross-references: GB:S79263; NID:q1086954; PID:AA35068.1; PID:q1086955
C:Genetics:
A:Gene: rIL-3beta
A:Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
C:Keywords: cytokine receptor
F:39-235/Domain: cytokine receptor homology <CRS1>
F:253-433/Domain: cytokine receptor homology <CRS2>

Query Match 13.6%; Score 162.5; DB 2; Length 896;
Best local Similarity 25.1%; Pred. No. 2.3e-06;
Matches 59; Conservative 32; Mismatches 89; Indels 55; Gaps 9;

QY 4 LVGYNDYLTQTVICILEMNLHPSTLTLT--WDOYEELDEATCSL----- 48
| | | | | : | | : | | |
Db 37 LQCYNDYLTERTICSWADTEDAOGVNLTLVHMD-----KKQPMSCSLSDLMWSECPSS 91
QY 49 HRSANNAHATYT-----CHMDVFHMDADIRSVNITDQSGVSESGSFLAASIKPAP 104
| | | | | : | | : | | |
Db 92 HNCVTRCVLPYTOPSVKEDYISLQDPDRSLHLV-----VPLAQHVQPPPP 139
QY 105 FNVYTFESG-QYNISWRSDEYDPAFYMLKGK-LQYELQYRNKGDPMAVSPRRKLISYDSR 162
| | | | | : | | : | | |
Db 140 KDISISPGDHFLKWSVPLGDAQVSLSKQDIOFEVAAYKQLODSWB-----DAS 189
QY 163 S-----VSLPLEFRKDSSELYQVRAGPMPGSGSYOGTSMSEWDPIYPTQSEEE 210
| | | | | : | | : | | |
Db 190 SLHTCNLWVTLPEPKLFLPNSTLYVARVRAQLAPGSSLSGRSGMSPEVHMSPTED 244

RESULT 2
A40091
interleukin-3 receptor beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: A40091; A43022
R:Itch, N.; Yonehara, S.; Schreurs, J.; Gorman, D.M.; Maruyama, K.; Ishii, A.; Yahara
Science 247, 324-327, 1990

A:Title: Cloning of an interleukin-3 receptor gene: a member of a distinct receptor gene
 A:Reference number: A40091; MUID:90117145
 A:Accession: A40091
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-878 <ITO>
 R.Gorman, D.M.
 submitted to GenBank, November 1989
 A:Reference number: A43022
 A:Accession: A43022
 A:Molecule type: mRNA
 A:Residues: 1-815, 'Q', 817-878 <GOR>
 A:Cross-references: GB:M29855; NID:9198342; PIDN:AAA9295.1; PID:9309406
 C:Comment: In mice there are two classes of high-affinity IL-3 receptors. One contains 2 receptors.
 C:Superfamily: Interleukin-3 receptor beta chain; cytokine receptor homology
 C:Keywords: cytokine receptor; duplication; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-878/Product: Interleukin-3 receptor beta chain #status predicted <MAT>
 F:23-440/Domain: extracellular #status predicted <EXT>
 F:39-236/Domain: cytokine receptor homology <CRS1>
 F:54-433/Domain: cytokine receptor homology <CRS2>
 F:41-462/Domain: transmembrane #status predicted <TM>
 F:463-878/Domain: intracellular #status predicted <INT>

Query Match 12.1%; Score 145; DB 1; Length 878;
 Best Local Similarity 23.0%; Pred. No. 8.3e-05;
 Matches 54; Conservative 30; Mismatches 91; Indels 60; Gaps 9;

QY 4 LVCTITLQVTCILEMNLHSTLTITWQD-----YEL-KDEATGCSL-- 48
 Db 37 LECYNDYTRITD-----SWADPEDAGLIMTLVHQLDKIQSVSCETSE 82
 QY 49 -----HRSANHATATYTCNM---DYFHEMADDFIVNTDQSGNYSQCGSFL 94
 Db 83 KLMMSCSPSSHRVRCVPIYTRFNGNDYYSFQPDLDLQI-----MVP 130
 QY 95 LAESIRPAPPNTVTFSG-QYNISWRSDYEDPAFYMKGR-LQYELQYRNQDPMAVSP 152
 Db 131 LACHVPPPPKDIHISPSDHFLEWVSILGDSOVSWLSSKIDFEVAVYKRIQDSWEDA- 189
 QY 153 RRLKIVDSRSVSLPLFRKDSYELQVRAGMPGSSYQGTWSPDPVIRQTQ 207
 Db 190 --SSLHTSNQVNLKPLFNPSTIARVTRLSAGSSLSGRPSRMSPVHMDSQ 242

RESULT 3

S68441
 A:Title: Leptin receptor, splice form Ob-Re - mouse
 A:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-2000 #sequence, revision 31-Dec-2000 #text, change 31-Dec-2000
 C:Accession: S68441
 R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; Fraz
 Nature 379, 632-635, 1996
 A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
 A:Reference number: S68437; MUID:96231997
 A:Accession: S68441
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-805 <LEE>
 A:Cross-references: EMBL:049110; NID:91195492; PIDN:AGS2424.1; PID:91195493
 A:Experimental source: splice form Re; tissue hypothalamus
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:S68439, PIR:S68439
 C:Genetics:
 A:Gene: Ob-Re
 C:Keywords: alternative splicing; appetite

Query Match 12.1%; Score 144; DB 2; Length 805;
 Best Local Similarity 31.1%; Pred. No. 9.1e-05;
 Matches 57; Conservative 22; Mismatches 60; Indels 44; Gaps 11;

QY 39 LKDE---ATSCSLHRSANHATATYTCMHDYFH-----FMADDISVNTDQSGNYS 87
 Db 177 LKDSFQVQNCNCSLRG-----ECHVPVPRALNTALMYLETITSAGVSFQSPILMS 227
 QY 88 QEGCSFLIASIRPAPP--FNVTTFSGQYNISWRSDYEDPAFYMKGR-LQYELQYRNNG 145
 Db 228 LQ--PMLV---VAPDPLGLHMEVTDGNLKSIMDSQTAPF-----PLQYQVATLENS 276
 QY 146 DPMVSPRRKLIVDSRSV-SLLPLFRKDSYELQVRAGMPGSSYQGTWSPDPVIR 204
 Db 277 T--IVRAAETIVATSLIVDSVLP-----GSSYEVQVRSKRLDGS---GVMSDMSPPQVF 326
 QY 205 QTO 207
 Db 327 TTTQ 329

RESULT 4

S68439
 A:Title: Leptin receptor, splice form Ob-Rc - mouse
 A:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-2000 #sequence, revision 31-Dec-2000 #text, change 31-Dec-2000
 C:Accession: S68439; S68441
 R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
 Nature 379, 632-635, 1996
 A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
 A:Reference number: S68437; MUID:96231997
 A:Accession: S68439
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 664-892 <LEE1>
 A:Cross-references: EMBL:049108; NID:91195488; PIDN:AGS2422.1; PID:91195489
 A:Experimental source: splice form Rc; tissue hypothalamus
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 A:Accession: S68441
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-796, GCMTVLPMW, <LEE2>
 A:Cross-references: EMBL:049110; NID:91195492; PIDN:AGS2424.1; PID:91195493
 A:Experimental source: splice form Re; tissue hypothalamus
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
 C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:
 C:Genetics:
 A:Gene: Ob-Rc
 C:Keywords: alternative splicing; appetite

Query Match 12.1%; Score 144; DB 2; Length 892;
 Best Local Similarity 31.1%; Pred. No. 0.0001;
 Matches 57; Conservative 22; Mismatches 60; Indels 44; Gaps 11;

QY 39 LKDE---ATSCSLHRSANHATATYTCMHDYFH-----FMADDISVNTDQSGNYS 87
 Db 177 LKDSFQVQNCNCSLRG-----ECHVPVPRALNTALMYLETITSAGVSFQSPILMS 227
 QY 88 QEGCSFLIASIRPAPP--FNVTTFSGQYNISWRSDYEDPAFYMKGR-LQYELQYRNNG 145
 Db 228 LQ--PMLV---VAPDPLGLHMEVTDGNLKSIMDSQTAPF-----PLQYQVATLENS 276
 QY 146 DPMVSPRRKLIVDSRSV-SLLPLFRKDSYELQVRAGMPGSSYQGTWSPDPVIR 204
 Db 277 T--IVRAAETIVATSLIVDSVLP-----GSSYEVQVRSKRLDGS---GVMSDMSPPQVF 326
 QY 205 QTO 207
 Db 327 TTTQ 329

RESULT 5

S68437
 A:Title: Leptin receptor, splice form Ob-Ra - mouse

Query Match	12.1%	Score 144;	DB 2;	length 1162;
Best Local Similarity	31.1%	Pred. No. 0.00015;		
Best Local				
Matches 57;	Conservative 22;	Mismatches 60;	Indels 44;	Gaps 11;

Qy	1KDE	-----ATSCSLRSHAMNAHATVTCGMDFH-----	-----MADDIFFVNITDSCGN	87
	39			
Db	177	LKDSQYQVQCNSLGC-----	-----ECHVPYPRAKLTALLMYLEITSAGVSFOSPLMS	227
	88	QEGCSFLLAESIKPAPP--FNVTVFESGOYNISWRSDEDPAPFMYMKGLQYELQYRNRG	145	
Qy	228	LQ--PMLV--VKRPPPLGLHMEYVDGGLKLSMSQYMAP-----	-----PLOQYQYKLEMS	276
	146	DEWAVSPRRKLTIVDSRSY--SLLPLEFRKDSYELQVRAGPMPGSSYQGTWSEMSDPVTE	204	
Db	277	T--IVRAEAETIVATSLAVDSVLP-----	-----GSSYEYQVRSKRLEDGS---GWSMDWSSQYVE	326
Qy	205	QTQ 207		
	327	TTQ 329		

RESULT 9
A35052
Interleukin-2 receptor beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 05-Nov-1999
C:Accession: A35052
R:Kono, T.; Doi, T.; Yamada, G.; Hatakeyama, M.; Minamoto, S.; Tsudo, M.; Miyasaka, M.;
Proc. Natl. Acad. Sci. U.S.A. 87, 1806-1810, 1990
A:Title: Murine interleukin-2 receptor beta chain: dysregulated gene expression in lymphoma
X:Reference number: A35052; MUID:90175385
Accession: A35052

Query Match	11.8%	Score 141.5	DB 2	Length 539
Best Local Similarly	22.58%	Pred. No. 9.1e-05		
Matches 54; Conservative	43;	Mismatches 86;	Indels 57;	Gaps 12

```

0Y 1 CPDLVCYNDYDLOTVCICILEMNLHSTLTLLTMQDQEEELKDATGCSLHRSNNHTHAY 60
Db 31 CSHECCFNSTRANVSC---MWS-HEEALNV-----TTCYHAKS-NLRHMK 72
0Y 61 TCHMDVFH-----FMADIFSVNIT--DQSGNVOECGSFLLAESIK 100
Db 73 TCCELLVQAQSMACNLLIGSPESQSLTSVDLLDINVCMEKGRNRVTCDFHPFDNIR 132
0Y 101 PAPERNTVTF--SGQYNISWR---SDYEDEAFYMLGKIOLEYOYRRNRGDPMAVSPRR 154

```

```

Db      133  LVAPHISLOYLHIDTQRCNISMKNVQSVMHPIEP-----YLEFARRKLLGHSMEDA--- 182
QY      155  KLISVDSRSVSLPLPEFFKKDSYELQVRAGMPCSSYQGTMSKSDPVIQTQI-SEELKE 213
      183  SVLSLAKQKQKQKQKLEMLIPSTSYEVQKRVKQKRRNT--GTMSPSPSQGLFRTIRTRADPMKE 240

```

RESULT 10
B45266
MPL-k protein precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
C:Accession: B45266
R:Vison, I.; Mornon, J.P.; Cocault, L.; Mitjavila, M.T.; Tambourin, P.; Gisselbrecht, P.; Proc. Natl. Acad. Sci. U.S.A. 89, 5640-5644, 1992
A:Title: Molecular cloning and characterization of MPL, the human homolog of the v-mpl
A:Reference number: A45266; MUID:92302297
A:Accession: B45266
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-579 <VIG>
A:Cross-references: GB:M90103; NID:g184262; PIDN:AAA69972.1; PID:g184263

	Query Match	11.6%	Score 139;	DB 2:	Length 579;	
	Best Local Similarity	24.0%;	Pred. No. 0.00017;			
	Matches	59;	Conservative	25;	Mismatches	76; Indels 86; Gaps 14;
OY	4	IVCYDYDQTQVLCILMMNLHPSTLTLLTWODQYEELKEATSCSL--HRSAHNATHATY- 60				
		: : :	: : :			
Db	289	LQCFLDLKKNVTC-----QMQQQ-----DHASSQGFFHYHRACCPDRDPY 329				
OY	61	-----TCHM-----DVFNHMADDFESVNTIDSGNSIQEGCS-F 93				
		: : :	: : :			
Db	330	IWENCEEEKTNPGIQTPOFSRCHNRSDSIITHL-----VEYTTAGTVHSTLGSF 363				
OY	94	LVAEIR-PAPFPNTVTFSGQYNISWRSDYDDPAFYMLKGRLQLOLRNG-DPWAYS 151				
		: : : : : : :	: : : : : : :			
Db	384	WHQAVRLPTPLMHREISSGHLEDEM---QHPSMAAQ-ETCYQLRYTGEGHDMKV- 437				
OY	152	PRKKLIVDSKSVSLP-----LEFKDSSYLEQVAGCMPPSSVQGTSEMSDPI 203				
		: : : :	: : : :			
Db	438	-----LEPPLGARGGLTELPKRRYRIQLA-PLNPQTYOGPMSSWDPR 482				

```

Oy      204  F0T0SE  209
       :  :  :
Db      483  VETATE 488

RESULT  11
A45266
MPL-P protein precursor - human
C:Species: Homo sapiens (man)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
C:Accession: A45266
R:Vison, I.; Mornon, J.P.; Coccault, L.; Mitjavila, M.T.; Tambourin, P.; Gisselbrecht,
Proc. Natl. Acad. Sci. U.S.A. 89, 5640-5644, 1992
A:Title: Molecular cloning and characterization of MPL, the human homolog of the v-mp
A:Reference number: A45266; MUID:92302297
A:Accession: A45266
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-635 <VIG>
A:Cross-references: GB:M90102; NID:g184260; PIDN:AAA69971.1; PID:g184261
;Keywords: transmembrane protein

```

Query Match	11.6%;	Score 139;	DB 2;	Length 635;
Best Local Similarity	24.0%;	Pred. No. 0.00019;		
Matches	59; Conservative	25; Mismatches	76; Indels	86; Gaps 14;
OY	4	LVCYDYDQVYCIILMMNHPSTLTLLWODYYEELKDEATSCSL--HRSANNTHATAY-	60	
I	:	I	:	I
:	:	:	:	:

RESULT 14
A60386
interleukin-4 receptor precursor - human
N:Alternate names: IL-4 receptor
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: A60386; A47603
R:Galizai, J.P.; Zuber, C.E.; Harada, N.; Gorman, D.M.; Djossou, O.; Kastelein
Int. Immunol. 2, 669-675, 1990
A:Title: Molecular cloning of a cDNA encoding the human interleukin 4 receptor
A:Reference number: A60386; MUID:91120547
A:Accession: A60386
A:Status: not compared with conceptual translation
A:Molecule type: mRNA

A:Residues: 1-825 <GAL>
 R:Idzerda, R.L.; Match, C.J.; Mosley, B.; Lyman, S.D.; Vanden Bos, T.; Gimpel, S.D.; Ditt
 J. Exp. Med. 171, 861-873, 1990
 A:Title: Human Interleukin 4 receptor confers biological responsiveness and defines a nc
 A:Reference number: A47603; MUID:90171849
 A:Accession: A47603
 A:Molecule type: mRNA
 A:Residues: 1-74, '1', 76-825 <ID2>
 A:Cross-references: GB:X52425; NID:933833; PIDN:CAA3672.1; PID:933834
 C:Genetics:
 A:Gene: GDB:IL4R
 A:Cross-references: GDB:118823; OMIM:147781
 A:Map position: 16p12.1-16p12.1
 C:Superfamily: Interleukin-4 receptor; cytokine receptor homology
 C:Keywords: cytokine receptor; glycoprotein; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-825/Product: Interleukin-4 receptor #status predicted <MAT>
 F:26-232/Domain: extracellular #status predicted <EXT>
 F:34-218/Domain: cytokine receptor homology <CRS>
 F:23-256/Domain: transmembrane #status predicted <TM>
 F:237-825/Domain: intracellular #status predicted <INT>
 F:3, 98, 128, 134, 176, 209/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.3%; Score 135.5; DB 1; Length 825;
 Best Local Similarity 26.0%; Pred. No. 0.00054;
 Matches 57; Conservative 25; Mismatches 76; Indels 61; Gaps 12;

QY 6 CYTDYLTQYICILEMNLHPST-----LTLTWQDYELKDEKSCSLHSAHNAHTATY 60
 Db 34 CVDYMSISTC---EWMKNGPTNCSTELRYLYQVLF--LLEAHNC---VPENNAGAGC 84
 QY 61 TCHWDVHFMAADDFSVNITDQSGNYSOEC-----GSFLAESIKAPPFNTVY-- 109
 Db 85 VCHL-----LMDVVSAD-----NTLDIMAGQQLMKGSEKPSRHVPRAPGNLTVHT 133
 QY 110 TFSQYINISRSYEDPAFYMLKGLQYELQYRNRGDPMAVSPRRKLISVDSRSVSLPL 169
 Db 134 NVSDTLTLTWSNPY--PPDNYLYNHLTYAVNIWSENP-----ADFRIVNVTYL 180
 QY 170 E-----FRKDSYELQVRAGPMPGSSYOGTSEMS 199
 Db 181 EPSLRITASTLKSGISIRARVRAM---AOCYNTTWSEMS 216

RESULT 15
 B46535
 Interleukin 2 receptor beta chain - rat
 C:Species: Rattus norvegicus (Norway rat)
 A:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jun-2000
 A:Accession: B46535
 R:Page, T.H.; Dailman, M.J.
 Eur. J. Immunol. 21, 2133-2138, 1991
 A:Title: Molecular cloning of cdnas for the rat interleukin 2 receptor alpha and beta ch
 A:Reference number: A46535; MUID:91364784
 A:Accession: B46535
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-537 <PAG>
 A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBIN:60818, NCBIPI:60819)
 C:Superfamily: fibronectin type III repeat homology
 C:Keywords: cytokine receptor

Query Match 11.2%; Score 134; DB 2; Length 537;
 Best Local Similarity 23.1%; Pred. No. 0.00042;
 Matches 58; Conservative 41; Mismatches 72; Indels 80; Gaps 13;

QY 1 CPDLVCTDYLTQYICILEMNLHPSTLTLTWQDYELKDEA---TSCSLHSAH----- 53
 Db 31 CSHLKCFYNSRANVSC---WMS-----PEPALNVTSCIHAKSDMRHW 70

QY 54 NAT-----HATYCHM-----DVHFMAADDFSVNIT--DQSGNYSOECGSLAES 98
 Db 71 NKCCCLPVAQASMACNLLIGPLPDQSLSVSLVSCWEKGRVKTCHNHPDN 130
 QY 99 IKPAPPNNTVYTF--SGQYNISNR-----SDYEDPAFYMLKGLQYELQYRNRGDPMAVSP 152
 Db 131 LRLTAPHSILOVLIETRRCNISWESQVSHVYNP-----YLFEE-----A 170
 QY 153 RRKLISVDSRSVSLPLLEFRK-----DSYELQVRAGPMPGSSYOGTSEMSDPV 202
 Db 171 RRRLLDSWEDASVFLKQKQGWIFLETLPPTSYELQVRVIAQGKT--RTWSPWSPM 228
 QY 203 IFOTOSSEELKE 213
 Db 229 AFRTRPADPRE 239

Search completed: June 28, 2002, 07:42:53
 Job time: 128 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2002, 07:40:45 ; Search time 110.69 Seconds
(without alignments)
232.804 Million cell updates/second

Title: US-09-825-561A-4
Perfect score: 1288
Sequence: 1 LNTTILPFGNEDTTADFFL.....QHSEWSHPITHGSNTSKEN 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
total number of hits satisfying chosen parameters: 747574

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database : A_Geneseq_032802.*

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2:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1981.DAT.*
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7:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1986.DAT.*
8:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1987.DAT.*
9:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1988.DAT.*
10:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1989.DAT.*
11:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1990.DAT.*
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13:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1992.DAT.*
14:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1993.DAT.*
15:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1994.DAT.*
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17:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1996.DAT.*
18:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1997.DAT.*
19:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA2001.DAT.*

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	1288	100.0		347	15	AAR47149	IL-2 receptor gamma
2	1288	100.0		369	15	AAR47148	IL-2 receptor gamma
3	1288	100.0		691	21	AAV93202	Fusion polypeptide
4	1288	100.0		694	21	AAV93201	Fusion polypeptide
5	1288	100.0		694	21	AAV93203	Fusion polypeptide
6	1282	99.5		482	19	AAW31646	Human cytokine rec
7	1277	99.1		230	15	AAR47150	IL-2 receptor gamma
8	1277	99.1		252	15	AAR47151	IL-2 receptor gamma
9	1272	98.8		330	16	AAR82934	Interleukin 4 comp
10	960	74.5		363	22	AAB71682	Mus taupus interle
11	854.5	66.3		369	15	AAR59094	Murine IL-2R gamma

1	542	42.1	121	21	AAUG0283	Human secreted protein
12	215	16.7	561	22	AAUG69138	Canine IL-13Ralpha
13	215	16.7	561	22	AAUG69141	Canine IL-13Ralpha
14	215	16.7	561	22	AAUG69140	Canine IL-13Ralpha
15	215	16.7	563	22	AAUG69139	Canine IL-13Ralpha
16	215	16.7	563	22	AAUG69137	Canine IL-13R extrin
17	213	16.5	518	22	AAUG69136	Canine interleukin
18	213	16.5	365	22	AAUG69135	Canine interleukin
19	207	16.1	316	19	AAUG69135	Canine interleukin
20	207	16.1	355	19	AAUG69135	Canine interleukin
21	207	16.1	359	19	AAUG69135	Canine interleukin
22	207	16.1	380	18	AAUG69135	Canine interleukin
23	207	16.1	380	18	AAUG69135	Canine interleukin
24	207	16.1	380	18	AAUG69135	Canine interleukin
25	207	16.1	380	18	AAUG69135	Canine interleukin
26	207	16.1	380	19	AAUG69135	Canine interleukin
27	207	16.1	380	19	AAUG69135	Canine interleukin
28	207	16.1	380	21	AAUG69135	Canine interleukin
29	207	16.1	380	21	AAUG69135	Canine interleukin
30	207	16.1	380	22	AAUG69135	Canine interleukin
31	207	16.1	380	22	AAUG69135	Canine interleukin
32	206	16.0	255	22	AAUG69134	Canine interleukin
33	205	15.8	380	18	AAUG69134	Canine interleukin
34	199.5	15.5	383	18	AAUG69134	Canine interleukin
35	199.5	15.5	383	21	AAUG69134	Canine interleukin
36	199.5	15.5	383	22	AAUG69134	Canine interleukin
37	199.5	15.5	383	22	AAUG69134	Canine interleukin
38	183.5	14.2	372	18	AAUG69134	Canine interleukin
39	180	14.0	426	18	AAUG69134	Canine interleukin
40	178	13.8	426	18	AAUG69134	Canine interleukin
41	178	13.8	427	18	AAUG69134	Canine interleukin
42	178	13.8	427	22	AAUG69134	Canine interleukin
43	178	13.8	427	22	AAUG69134	Canine interleukin
44	178	13.8	784	21	AAUG69134	Canine interleukin
45	178	13.8	793	21	AAUG69134	Canine interleukin

ALIGNMENTS

RESULT	1
ID	AAR47149
XX	AAR47149 standard; Protein; 347 AA.
AC	
XX	AAR47149;
DT	13-JUN-1994 (first entry)
XX	
DE	IL-2 receptor gamma chain.
XX	
KW	Interleukin-2 receptor gamma chain; IL-2; receptor; immunoregulator
KW	rheumatoid arthritis; transplant rejection; primer;
KW	polymerase chain reaction; PCR; amplification.
OS	Homo sapiens.
XX	
PN	EP578932-A.
PD	19-JAN-1994.
PF	22-APR-1993; 93EP-0106561.
PR	23-APR-1992; 92JP-0104947.
PA	(AJIN) AJINOMOTO KK.
PA	(SUGA/) SUGAMURA K.
PI	Akao H, Hamuro J, Nakamura M, Shimamura T, Sugamura K;
PI	Suzuki M, Takeshita T;
DR	WPI; 1994-017546/03.
DR	N-PDB; AAO54829.
XX	
XX	DNA and protein sequences of IL-2 gamma chain - useful as immune

DR N-PSDB; AAA09044.

XX Isolated nucleic acid molecule for treating cytokine-related diseases
PT or disorders encodes a fusion polypeptide capable of binding a cytokine
PT to form a nonfunctional complex

XX Example 6; Fig 22A-D; 152pp; English.

XX This sequence shows fusion polypeptide 603, which is capable of
CC binding cytokine IL-4 to form a non-functional complex.
CC The invention concerns production of antagonists to any cytokine that
CC utilizes an alpha specificity determining component, which when combined
CC with the cytokine, binds to a first beta signal transducing component to
CC form a non-functional intermediate which then binds to a second beta
CC signal transducing component causing beta-receptor dimerization, the
CC soluble alpha specificity determining component of the receptor
CC (SR-alpha) and the extracellular domain of the first beta signal
CC transducing component of the cytokine receptor (beta-1) are combined to
CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
CC cytokine by binding the cytokine to form a non-functional complex. The
CC receptor components are shared by cytokines such as the CNTF (ciliary
CC neurotrophic factor) family of cytokines. The invention provides the
CC basis for the development of IL-6 antagonists, as they show that if, in
CC the presence of a ligand, a non-functional intermediate complex, consisting
CC of the ligand, its alpha receptor and its beta-1 receptor
CC component, can be formed, it will effectively block the action of the
CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
CC of the extracellular domains of the alpha specificity determining
CC components of their receptors and the extracellular domain of gp130.
CC The resultant heterodimers, function as high-affinity traps, rendering
CC the cytokine inaccessible to form a signal transducing complex with the
CC native membrane-bound forms of their receptor. The nucleic acids and
CC polypeptides are useful for treating cytokine-related diseases or
CC disorders such as osteoporosis and primary and secondary effects of
CC cancer including multiple myeloma or cachexia.

XX Sequence 691 AA:

SQ
Query Match 100.0%; Score 1288; DB 21; Length 691;
Best Local Similarity 100.0%; Pred. No. 1.8e-115;

Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTLTPNGNEDTADFFLTPTDLSVSTLPLPEVOCFVNEVMNCTMNSSEPP 60

DB 23 Inttltpngnedtadffltptdlsvstlplpevcfvevmnctwnssepp 82

QY 61 TNLTLHWYKNSDNDKVKQCSHYLFSEETISGCOLKKEIHLYOTFYVOLQDRPRRQA 120

DB 83 TNLTLHWYKNSDNDKVKQCSHYLFSEETISGCOLKKEIHLYOTFYVOLQDRPRRQA 142

QY 121 TQMLKQLNLYIPWAPENLTLHKLSQSLELNMNRRFLNHCLEHLVQYRTDMDHSWTQSGV 180

DB 143 TQMLKQLNLYIPWAPENLTLHKLSQSLELNMNRRFLNHCLEHLVQYRTDMDHSWTQSGV 202

QY 181 DYRHKFSLPSVDGQKRYTFVRVSRFPNPLCGSAOHMSEMSHP IHMGSNTSKEN 232

DB 203 DYRHKFSLPSVDGQKRYTFVRVSRFPNPLCGSAOHMSEMSHP IHMGSNTSKEN 254

RESULT 4

AA92201

ID AA92201 standard; Protein; 694 AA.

XX AA92201;

XX 01-AUG-2000 (first entry)

XX Fusion polypeptide 424, IL-4 trap.

XX IL-4 trap; cytokine; antagonist; CNTF; receptor; fusion protein;

KM Cytostatic; Immunomodulator; osteopatinic.

XX

OS Synthetic.

OS Homo sapiens.

PN WO200018932-A2.

PD 06-APR-2000.

PF 22-SEP-1999; 99WO-US22045.

PR 25-SEP-1998; 98US-0101858.

PR 19-MAY-1999; 99US-0313942.

PA (REGG-) REGENERON PHARM INC.

PI Stahl N, Yancopoulos GD;

DR WPI: 2000-293165/25.

DR N-PSDB; AAA09043.

PT Isolated nucleic acid molecule for treating cytokine-related diseases
PT or disorders encodes a fusion polypeptide capable of binding a cytokine
PT to form a nonfunctional complex

XX Example 6; Fig 21; 152pp; English.

XX This sequence shows fusion polypeptide 424, which is capable of
CC binding cytokine IL-4 to form a non-functional complex.
CC The invention concerns production of antagonists to any cytokine that
CC utilizes an alpha specificity determining component, which when combined
CC with the cytokine, binds to a first beta signal transducing component to
CC form a non-functional intermediate which then binds to a second beta
CC signal transducing component causing beta-receptor dimerization, the
CC soluble alpha specificity determining component of the receptor
CC (SR-alpha) and the extracellular domain of the first beta signal
CC transducing component of the cytokine receptor (beta-1) are combined to
CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
CC cytokine by binding the cytokine to form a non-functional complex. The
CC receptor components are shared by cytokines such as the CNTF (ciliary
CC neurotrophic factor) family of cytokines. The invention provides the
CC basis for the development of IL-6 antagonists, as they show that if, in
CC the presence of a ligand, a non-functional intermediate complex,
CC consisting of the ligand, its alpha receptor and its beta-1 receptor
CC component, can be formed, it will effectively block the action of the
CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers
CC of the extracellular domains of the alpha specificity determining
CC components of their receptors and the extracellular domain of gp130.
CC The resultant heterodimers, function as high-affinity traps, rendering
CC the cytokine inaccessible to form a signal transducing complex with the
CC native membrane-bound forms of their receptor. The nucleic acids and
CC polypeptides are useful for treating cytokine-related diseases or
CC disorders such as osteoporosis and primary and secondary effects of
CC cancer including multiple myeloma or cachexia.

SQ Sequence 694 AA:

Query Match 100.0%; Score 1288; DB 21; Length 694;
Best Local Similarity 100.0%; Pred. No. 1.8e-115;

Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTLTPNGNEDTADFFLTPTDLSVSTLPLPEVOCFVNEVMNCTMNSSEPP 60

DB 23 Inttltpngnedtadffltptdlsvstlplpevcfvevmnctwnssepp 82

QY 61 TNLTLHWYKNSDNDKVKQCSHYLFSEETISGCOLKKEIHLYOTFYVOLQDRPRRQA 120

DB 83 TNLTLHWYKNSDNDKVKQCSHYLFSEETISGCOLKKEIHLYOTFYVOLQDRPRRQA 142

QY 121 TQMLKQLNLYIPWAPENLTLHKLSQSLELNMNRRFLNHCLEHLVQYRTDMDHSWTQSGV 180

DB 143 TQMLKQLNLYIPWAPENLTLHKLSQSLELNMNRRFLNHCLEHLVQYRTDMDHSWTQSGV 202

QY 181 DYRHKFSLPSVDGQKRYTFVRVSRFPNPLCGSAOHMSEMSHP IHMGSNTSKEN 232

|||||
 Db 203 dyrhkfslpsvdgqkrylfrvrsrfrnplcgsgqhwsewshp1ngsntskn 254

RESULT 5
 ID AAY92203 standard; Protein; 694 AA.
 XX
 AC AAY92203;
 XX
 DT 01-AUG-2000 (first entry)
 DE Fusion polypeptide 622, IL-4 trap.
 XX
 DE Fusion polypeptide 622, IL-4 trap.
 XX
 KM IL-4 trap; cytokine; antagonist; CMF; receptor; fusion protein;
 XX cytostatic; immunomodulator; osteopathic.
 OS Synthetic.
 OS Homo sapiens.
 OS

W0200018932-A2.

PD 06-APR-2000.
 XX 22-SEP-1999: 99WO-US22045.
 XX
 PR 25-SEP-1998: 98US-0101858.
 PR 19-MAY-1999: 99US-0313942.
 PA (REG-) REGENERON PHARM INC.
 PI Stahl N, Yancopoulos GD;
 XX
 DR WPI: 2000-293165/25.
 DR N-PSDB; AAA9045.
 XX
 PT Isolated nucleic acid molecule for treating cytokine-related diseases
 PT or disorders encodes a fusion polypeptide capable of binding a cytokine
 PT to form a nonfunctional complex
 XX
 PS Example 6; Fig 23A-D; 152pp; English.
 XX

CC This sequence shows fusion polypeptide 622, which is capable of
 CC binding cytokine IL-4 to form a non-functional complex.
 CC The invention concerns production of antagonists to any cytokine that
 CC utilizes an alpha specifically determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specificity determining component of the receptor
 CC (SR-alpha) and the extracellular domain of the first beta signal
 CC transducing component of the cytokine receptor (beta-1) are combined to
 CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the
 CC cytokine by binding the cytokine to form a non-functional complex. The
 CC receptor components are shared by cytokines such as the CMF (ciliary
 CC neurotrophic factor) family of cytokines. The invention provides the
 CC basis for the development of IL-6 antagonists, as they show that if, in
 CC the presence of a ligand, a non-functional intermediate complex,
 CC consisting of the ligand, its alpha receptor and its beta-1 receptor
 CC component, can be formed, it will effectively block the action of the
 CC ligand. Effective antagonists of IL-6 or CMF consist of heterodimers
 CC of the extracellular domains of the alpha specificity determining
 CC components of their receptors and the extracellular domain of gp130.
 CC The resultant heterodimers, function as high-affinity traps, rendering
 CC the cytokine inaccessible to form a signal transducing complex with the
 CC native membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia.
 CC
 XX
 SQ Sequence 694 AA;

Query Match 100.0%; Score 1288; DB 21; Length 694;
 Best Local Similarity 100.0%; Pred. No. 1,86-115;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILPENGNETTADFTLTPTDLSVTLPLPEVOCFVFNWYKNCWNSSEPPQ 60
 DB 23 Intlltpngnedttdadftltptdls1svstlplpevcfivfeygmctwnssseppq 82
 QY 61 TNLTLHWYKNSDNDKYQKCSHYLFSEITSGGQLOKKEIHLHYQFVVOLODPPRPPQA 120
 DB 83 tnltlhwynsdndkyqkcschy1fseeltsqgqlqkkeh1hyqfivvqlqdprrppq 142
 QY 121 TQMLKIQNLVTPWAPENLTLHKLSOLEIMNNRFLNHCLEHLVQYRTDMDHKTQDSV 180
 DB 143 tqmklqnlvtpwapenl1lhklsesq1elnwnrflnhclehlyqyrtwdhswteqsv 202
 QY 181 DYRHKFSLPSVDGOKRYTFRVRSRFPPLCGSAOHMSEMSHP1HMSNTSKEN 232
 DB 203 dyrhkfslpsvdgqkrylfrvrsrfrnplcgsgqhwsewshp1ngsntskn 254

RESULT 6
 ID AAW31646 standard; Protein; 482 AA.
 XX
 AC AAW31646;
 XX
 DT 21-MAY-1998 (first entry)
 XX
 DE Human cytokine receptor gc chain-ig fusion protein.
 XX

XX Cytokine receptor; gamma common chain; gc chain; human;
 KM blocking agent; monoclonal antibody; CP.B8; immunological disease;
 KM myasthenia gravis; rheumatoid arthritis; lupus; multiple sclerosis;
 KM insulin-dependent diabetes; inflammatory bowel disease;
 KM sympathetic ophthalmia; uveitis; allergy; asthma; infection;
 KM graft versus host disease; psoriasis; immunosuppressive; therapy.
 XX
 OS Chimeric - Homo sapiens.
 XX

XX Key Location/Qualifiers
 FH Protein 1..254
 FT /note="gc chain N-terminal region"
 FT Protein 255..482
 FT /note="IgG1 constant region"
 FT Region 255..264
 FT /note="IgG1 hinge region"
 FT 264..482
 FT /note="IgG1 CH2 and CH3 constant domains1"
 XX

PN W09743416-A1.
 XX
 PD 20-NOV-1997.
 XX
 PF 09-MAY-1997: 97WO-US07870.
 XX
 PR 10-MAY-1996: 96US-0017466.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Benjamin CD, Burkly LC, Hession C, Whitty A;
 XX
 DR WPI: 1998-008885/01.
 DR N-PSDB; AAT97439.
 XX

PT Blocking agents of the gamma common chain of cytokine receptors -
 PT particularly monoclonal antibodies, used to induce T cell anergy for
 PT treatment of immunological diseases
 XX
 PS Example 1; Page 79-80; 11pp; English.
 XX

CC This polypeptide comprises a fusion between the N-terminal 254
 CC amino acids of the human mature cytokine receptor gamma common (gc)


```
XX DNA and protein sequences of IL-2 gamma chain - useful as immune
PT regulatory agents for treatment of e.g. rheumatoid arthritis and
PT transplant rejection
PS Disclosure; Page 21-22, 34-35; 50pp; English.
XX
CC The human IL-2 receptor gamma chain preform (AA047148), including the
CC signal peptide, is encoded by the sequence given in AA054828. The
CC mature protein (AA047149) is encoded by sequence AA054829. A soluble
CC form of IL-2 receptor gamma chain (AA047150) is encoded by AA054830.
CC while a soluble form suitable for expression in prokaryotes (AA047151)
CC is encoded by AA054831. Primers 1-6 (AA054820-25) are based on the N-
CC terminal sequence of IL-2 receptor gamma chain, and are used to
CC isolate IL2 receptor gamma chain receptor cDNA. Primers AA054826-27
CC are used to obtain the protein given in AA047151.
XX
SQ Sequence 252 AA:

Query Match 99.1%; Score 1277; DB 15; Length 252;
Best Local Similarity 100.0%; Pred. No. 4,9e-115;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNTTILTPNGNEEDTADFLTTMPDLSVSTLPLPEVQCFVFNENYKNCWTWSSSEPP 60
DB 23 Lnttliltpngnedtadflttmptdlsvstlplpevqcfvfnymctwsssepp 82
OY 61 TNLTLHWYKNSDNDKVQKCSHYLFSEETSGCOLQKKEIHLVQTFVYQLODPPRPRQA 120
DB 83 tnltlhwynsdndkvqkcshylfseetsgcqlkkeihlyqtfvvyqldppreprqa 142
OY 121 TOMKLQNLVTPAPENLTLAKLSSEQLLNMMNRFNLNHCLEHLVQYRTDMDHSWTQSV 180
DB 143 tqmklqnlvtpapenltlhklsesqlelnmmnrfnlnclehlvqyrtddhswtqsv 202
OY 181 DYRKFSLPVSDGOKRYTFVRSRFNPICGSAQHSEMSHPIMGSSNTS 230
DB 203 dyrhkfslpvsgokrytfvrstrfnpicgsaqhsewshpimwgsntsk 252

RESULT 9
AAR82934
ID AAR82934 standard; Protein; 230 AA.
XX
AC AAR82934;
XX
XX 26-FEB-1996 (first entry)
PT
XX Interleukin 4 component common to the IL-2 receptor gamma chain.
XX
KW Interleukin-4; IL-4; gamma chain component; immunosuppressants;
KW anti-allergy agent; signal transmsion inhibitor; autoimmune;
KW disease; anti-inflammatory; anaphylactic shock; bronchial asthma;
KW Interleukin-2; IL-2; atopic dermatitis; urticaria.
XX
OS Homo sapiens.
XX
XX JP07149662-A.
XX
PD 13-JUN-1995.
XX
XX 07-SEP-1994; 94JP-0213706.
XX
XX 08-SEP-1993; 93JP-0223574.
XX
XX (AJIN /) AJINOMOTO KK.
XX (SUGA /) SUGAMURA K.
XX
XX WPI; 1995-243601/32.
XX
XX N-PSDB; AAT04952.
XX
XX Novel interleukin-4 receptor monoclonal antibodies inhibit signal
PT
```

```
PT transmission - useful as immunosuppressants and anti-allergy agents.
XX
XX Example 1; Page 9; 11pp; Japanese.
PS
XX
CC AAT04952 encodes AAR82934 a component of the IL-4 receptor common to
CC the IL-2 receptor gamma chain molecule, which was used to generate
CC anti-IL-4 receptor monoclonal antibodies (mabs). The mabs (IL-4
CC signal transmission inhibitors) can be used as immunosuppressants
CC and anti-allergy agents, for the treatment of autoimmune and chronic
CC inflammatory diseases, e.g. anaphylactic shock, bronchial asthma,
CC atopic dermatitis and urticaria.
XX
XX
SQ Sequence 230 AA:

Query Match 98.8%; Score 1272; DB 16; Length 230;
Best Local Similarity 100.0%; Pred. No. 1,3e-114;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNTTILTPNGNEEDTADFLTTMPDLSVSTLPLPEVQCFVFNENYKNCWTWSSSEPP 60
DB 2 Lnttliltpngnedtadflttmptdlsvstlplpevqcfvfnymctwsssepp 61
OY 61 TNLTLHWYKNSDNDKVQKCSHYLFSEETSGCOLQKKEIHLVQTFVYQLODPPRPRQA 120
DB 62 tnltlhwynsdndkvqkcshylfseetsgcqlkkeihlyqtfvvyqldppreprqa 121
OY 121 TOMKLQNLVTPAPENLTLAKLSSEQLLNMMNRFNLNHCLEHLVQYRTDMDHSWTQSV 180
DB 122 tqmklqnlvtpapenltlhklsesqlelnmmnrfnlnclehlvqyrtddhswtqsv 181
OY 181 DYRKFSLPVSDGOKRYTFVRSRFNPICGSAQHSEMSHPIMGSSNTS 229
DB 182 dyrhkfslpvsgokrytfvrstrfnpicgsaqhsewshpimwgsntsk 230

RESULT 10
AAB71682
ID AAB71682 standard; protein; 363 AA.
XX
XX AAB71682;
XX
XX 10-MAY-2001 (first entry)
PT
XX Bos taurus interleukin-2 receptor gamma.
XX
XX
KW Cytokine receptor common gamma chain like; CRGGL; human;
KW tumours; infections; inflammatory; immune disorder;
KW neurodegenerative; cardiovascular; disorder.
XX
XX
OS Bos taurus.
XX
XX WO200112672-A2.
XX
XX 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US22493.
XX
XX 18-AUG-1999; 99US-0376430.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SA, Rosen CA, Moore PA;
XX
XX WPI; 2001-147547/15.
XX
XX New nucleic acid molecule encoding a human cytokine receptor common
XX gamma chain like polypeptide, useful for treating, preventing and/or
XX diagnosing e.g. tumors, inflammatory diseases and immunodeficiency
XX conditions -
XX
XX Disclosure; Fig 2; 288pp; English.
XX
```


XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
PS
XX Claim 13; SEQ ID 4364; 71pp + CD-ROM; English.

CC The present sequence is a polypeptide encoded by one of a large number
CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
CC were prepared from total human RNAs or polyA+ RNAs derived from 30
CC different tissues. EST sequences usually correspond mainly to the 3'
CC untranslated region (UTR) of the mRNA because they are often obtained
CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
CC those cases where longer cDNA sequences have been obtained, the full 5'
CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
CC ends and can therefore be used to obtain full length cDNAs and genomic
CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
CC chromosome mapping procedures. They are used to obtain upstream
CC regulatory sequences and to design expression and secretion vectors.

SQ Sequence 121 AA;

Query Match 42.1%; Score 542; DB 21; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.5e-44;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNTTILPNCNEDTADPFLTTMPTDLSVSTLPPEVOCFVFNVEYMNCTWNSSEPPQ 60
DB 23 LNTTILPNCNEDTADPFLTTMPTDLSVSTLPPEVOCFVFNVEYMNCTWNSSEPPQ 82
OY 61 TNLTLHWYKNSDNDKVKOKCSHYLFSEETISGCOLQKKE 99
DB 83 TNLTLHWYKNSDNDKVKOKCSHYLFSEETISGCOLQKKE 121

RESULT 13
AAU69138
ID AAU69138 standard; Protein; 561 AA.

AC AAU69138;

XX 29-JAN-2002 (first entry)

DE Canine IL-13Ralpha2/IgG-Fc fusion protein PcaIL-13Ralpha2-Fc-3523 561.

XX Dog: Interleukin-13 receptor alpha1; Interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KM Immunoglobulin light chain; lambda; Immunosuppressive; gene therapy;
immune response.

XX Canis familiaris.

OS WO200177332-A2.

XX 18-OCT-2001.

XX 09-APR-2001; 2001WO-US11498.

XX 07-APR-2000; 2000US-195659P.

PR 07-APR-2000; 2000US-195874P.

XX (HESK-) HESKA CORP.

XX McCall CA, Tang L;
PI MPI, 2001-657172/75.
DR N-PSDB; AAS59970.

XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -

XX Claim 46; Page 191-193; 221pp; English.

PS The invention concerns an isolated canine protein, preferably canine
XX immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13 proteins
CC and methods of isolating regulators in a canine. The regulators useful to
CC for regulating an immune response in a canine. The regulators useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13 mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence represents a protein of the invention.

SQ Sequence 561 AA;

Query Match 16.7%; Score 215; DB 22; Length 561;
Best Local Similarity 26.1%; Pred. No. 4.7e-12;
Matches 63; Conservative 37; Mismatches 103; Indels 38; Gaps 9;

OY 3 TTTLT-PNCNEDTADPFLTTMPTDLSVSTLPPEVOCFVFNVEYMNCTWNSSEPPQ-P 60
DB 105 TTYTSPGNGTET-----KIQDNDVYNNKYLVCWKPQMGVHFD 145
OY 61 TNLTLHWYKNSDNDKVKOKCSHYLFSEETISGCOLQKKEHLVOTFVQLODPRE--PRR 118
DB 146 TNYQIFYVEGIDHS--AECTDYIKVNGKMGCRFYLESDYKDFYICVNGSSEQPIR 203
OY 119 QATQMLKIQNVIVMAPENLTILHKLTSOLELMNN--NRFILNHCEHLVQYETDMDHSW 175
DB 204 PSYIFIGQIVKMPQYLSITVKNSEELIKWMPKGPAPAKCFIYELEFED-GLTW 262
OY 176 TEGSVYRHKFSLPSVDGQKRYRFRVSRFNPILGSAQHSEMSHPILHW-----GSN 227
DB 263 VTTVEVEIQITRTSNEQK-LCFIVRSKVNLYSDGSIWSEWSDQWKGDIWKETGSN 321
OY 228 T 228
DB 322 T 322

RESULT 14
AAU69141
ID AAU69141 standard; Protein; 561 AA.

AC AAU69141;

XX 29-JAN-2002 (first entry)

DE Canine IL-13Ralpha2/IgG-Fc fusion protein PcaIL-13Ralpha2-Fc-B9 561.

XX Dog: Interleukin-13 receptor alpha1; Interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KM Immunoglobulin light chain; lambda; Immunosuppressive; gene therapy;
immune response.

XX Canis familiaris.

OS WO200177332-A2.

XX 18-OCT-2001.

XX 09-APR-2001; 2001WO-US11498.

XX 07-APR-2000; 2000US-195659P.

PR 07-APR-2000; 2000US-195874P.

XX (HESK-) HESKA CORP.

[illegible]

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xx PF 09-APR-2001; 2001MO-US11498.
xx
xx 07-APR-2000; 2000US-195659P.
xx PR 07-APR-2000; 2000US-195874P.
xx
xx (HESK-) HESKA CORP.
xx
xx McCall CA, Tang L;
xx
xx WPI; 2001-657172/75.
xx DR N-PSDB; AAS59974.
xx
xx Novel isolated canine protein, preferably canine immunoglobulin G
xx protein or canine interleukin-13 receptor protein useful for regulating
xx immune response of an animal and for developing regulatory compounds -
xx
xx Claim 46; Page 203-206; 221pp; English.
xx
xx The invention concerns an isolated canine protein, preferably canine
xx immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
xx receptor protein, the nucleic acids encoding them, antibodies
xx raised against them, fusion proteins between the IgG and IL-13 proteins
xx and methods of isolating regulators of them. The regulators are useful
xx for regulating an immune response in a canine. The proteins useful to
xx develop regulatory compounds including inhibitors and activators that,
xx when administered to a canine in an effective manner, are capable of
xx protecting canine from disease mediated by IL-13alpha or IL-13. The
xx regulators are useful for treating canine IgG (heavy and/or light chain)
xx and/or canine IL-13R mediated responses. The molecules of the invention
xx are useful to regulate the immune response of an animal (e.g. by gene
xx therapy). The present sequence represents a protein of the invention.
xx
xx Sequence 563 AA:
xx
QY 3 TTILT-PNGNEDTDAFELTPTDLSLSTPLRLPEVOCFENVEYNNKSNSSSEPO-P 60
Db 105 tlytspgqiret-----kldmccyyymngylvswckpymgyhld 145
QY 16.7%; Score 215; DB 22; Length 563;
Best Local Similarity 26.1%; Pred. No. 4,7e-12;
Matches 63; Conservative 37; Mismatches 103; Indels 38; Gaps 9;
QY 3 TTILT-PNGNEDTDAFELTPTDLSLSTPLRLPEVOCFENVEYNNKSNSSSEPO-P 60
Db 105 tlytspgqiret-----kldmccyyymngylvswckpymgyhld 145
QY 61 TNLTLHWKNSDNDKVKQCSHYLSEETITSCQLQKKEHLVGTFFVVLQDPRE--PRR 118
Db 146 tnyllfyywagldhs--aectdyikngimgcrtfrylesedfyicvngssseqpr 203
QY 119 GATOMLKLQWLVYRNAPENILTLHKISEQGLNNWN---NRLNLCLEHLVOYGTDMDHSM 175
Db 204 psyflfdiqivfmpddyislcvknsseelnkmpkqriprackfilyelefted-gtvc 262
QY 176 TEQSVDRHNEFSLPSVDGQKRTYFRVRSNFNPLCGSAQMSWEMSHPIHW-----GSN 227
Db 263 vtlvnevelgtlrtnesqk-lcflvtrsvnlvycsdgdvweswdeqcmvkdwlketgpn 321
QY 228 T 228
Db 322 t 322

```

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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:40:45 ; Search time 20.33 Seconds

(without alignments)
441.856 Million cell updates/sec

Title: US-09-825-561A-4

Perfect score: 1288

Sequence: 1 LNTTTLTPNGNEDT7ADPFL.....QHNSKSPHFMGNTSKEN 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1288	100.0	369	1 CYRG_HUMAN	P31785 homo sapien
2	1097	85.2	373	1 CYRG_CANFA	P40321 canis fam11
3	990.5	76.9	379	1 CYRG_BOVIN	Q95118 bos taurus
4	853.5	66.3	369	1 CYRG_MOUSE	P34902 mus musculus
5	207	16.1	380	1 CYRG_MOUSE	Q14627 homo sapien
6	181.5	14.1	424	1 CYRG_MOUSE	Q09030 mus musculus
7	178	13.8	427	1 CYRG_MOUSE	P78552 homo sapien
8	159	12.3	897	1 CYRG_HUMAN	P32927 homo sapien
9	150	11.6	831	1 PRIR_CHICK	Q04594 gallus gall
10	146.5	11.4	400	1 GPCR_HUMAN	P15504 homo sapien
11	145.5	11.3	831	1 PRIR_MELGA	Q91094 melalegris g
12	132.5	10.3	830	1 PRIR_COLLI	Q90374 columba liv
13	132	10.2	810	1 ILAR_MOUSE	P16382 mus musculus
14	125	9.7	896	1 CYRG_MOUSE	P26955 mus musculus
15	121.5	9.4	581	1 PRIR_BOVIN	Q28172 bos taurus
16	118	9.2	415	1 IL5R_MOUSE	P26954 mus musculus
17	116	9.0	878	1 IL3B_MOUSE	P22272 mus musculus
18	114	8.9	460	1 IL6A_MOUSE	P22273 mus musculus
19	113	8.8	581	1 PRIR_CERL	Q02823 cervus elap
20	112	8.7	420	1 IL5R_HUMAN	Q01344 homo sapien
21	112	8.7	918	1 IL6B_HUMAN	P40189 homo sapien
22	110.5	8.6	551	1 IL2B_HUMAN	P40189 homo sapien
23	109.5	8.5	608	1 PRIR_MOUSE	Q08501 mus musculus
24	109	8.5	462	1 IL6A_RAT	P22273 mus musculus
25	108.5	8.4	610	1 PRIR_RAT	P05710 rattus norv
26	105	8.2	539	1 IL2B_MOUSE	P16297 mus musculus
27	105	8.2	1356	1 IL2B_MOUSE	Q03484 oncorhynch
28	104.5	8.1	917	1 IL6B_MOUSE	Q00560 mus musculus
29	104	8.1	1493	1 NEOL_MOUSE	P97798 mus musculus
30	102	7.9	611	1 GHR_COLLI	Q90375 columba liv
31	98.5	7.6	918	1 IL6B_RAT	P40190 rattus norv
32	97.5	7.6	467	1 IL6A_PIG	O18796 sus scrofa
33	97.5	7.6	608	1 GHR_CHICK	Q00092 gallus gall

ALIGNMENTS

RESULT 1	CYRG_HUMAN	STANDARD:	PRT:	369 AA.
AC P31785;				
DT 01-JUL-1993 (Rel. 26, Created)				
DT 01-JUL-1993 (Rel. 26, Last sequence update)				
DT 16-OCT-2001 (Rel. 40, Last annotation update)				
DE Cytokine receptor common gamma chain precursor (Gamma-C) (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64) (CD132 antigen).				
GN IL2RC.				
OS Homo sapiens (Human).				
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC Mammalia; Eulalia; Primates; Catarrhini; Homidae; Homo.				
OX NCBI_TaxID=9606;				
RN [1]				
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RX MEDLINE=92355883; PubMed=1631559;				
RA Takeshita T., Asao H., Ohtani K., Ishii N., Kumaki S., Tanaka N.,				
RA Munakata H., Nakamura M., Sugamura K.;				
RT "Cloning of the gamma chain of the human IL-2 receptor.";				
RL Science 257:379-382(1992).				
RN [2]				
RP SEQUENCE FROM N.A.				
RC TISSUE=Liver;				
RX MEDLINE=93293887; PubMed=8514792;				
RA Noguchi M., Adelstein S., Cao X., Leonard W.J.;				
RT "Characterization of the human Interleukin-2 receptor gamma chain gene.";				
RL J. Biol. Chem. 268:13601-13608(1993).				
RN [3]				
RP SEQUENCE FROM N.A., AND VARIANTS ASP-114 AND ASN-153.				
RX MEDLINE=94004847; PubMed=8401490;				
RA Puck J.M., Deschenes S.M., Porter J.C., Dutra A.S., Brown C.J.,				
RA Willard H., Henthorn P.S.;				
RT "The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-linked severe combined immunodeficiency, SCID1.";				
RL Hum. Mol. Genet. 2:1099-1104(1993).				
RN [4]				
RP IDENTIFICATION AS A IL-4R SUBUNIT.				
RX MEDLINE=94090315; PubMed=8266076;				
RA Kondo M., Takeshita T., Ishii N., Nakamura M., Watanabe S.,				
RA Arai K.-I., Sugamura K.;				
RT "Sharing of the interleukin-2 (IL-2) receptor gamma chain between RT receptors for IL-2 and IL-4.";				
RL Science 262:1874-1877(1993).				
RN [5]				
RP IDENTIFICATION AS A IL-4R SUBUNIT.				
RX MEDLINE=94090317; PubMed=8266078;				
RA Russell S.M., Kegan A.D., Harada N., Nakamura Y., Noguchi M.,				
RA Leonard P., Friedmann M.C., Miyajima A., Puri R.K., Paul W.E.,				
RT "Interleukin-2 receptor gamma chain: a functional component of the Interleukin-4 receptor.";				
RL Science 262:1880-1883(1993).				
RN [6]				
RP IDENTIFICATION AS A IL-7R SUBUNIT.				

34	97.5	7.6	825	1 IL4R_HUMAN	P24394 homo sapien
35	96.5	7.5	625	1 TPOR_MOUSE	Q08351 mus musculus
36	95.5	7.4	622	1 PRIR_HUMAN	P16471 homo sapien
37	95.5	7.4	630	1 PRIR_ORENI	Q91513 oreochromis
38	95.5	7.4	1461	1 NEOL_HUMAN	Q92859 homo sapien
39	95	7.4	312	1 F3ST_FLABI	P52835 flavaria bl
40	93	7.2	537	1 IL2B_RAT	P26896 rattus norv
41	92.5	7.2	1282	1 DOME_DROME	Q9VWE0 drosophila
42	92	7.1	508	1 EPOR_HUMAN	P19235 homo sapien
43	91.5	7.1	507	1 EPOR_MOUSE	P14753 mus musculus
44	91.5	7.1	1443	1 NEOL_CHICK	Q90610 gallus gall
45	91.5	7.1	1630	1 PRPL_DROME	P35992 drosophila

RX MEDLINE=94090316; PubMed=8266077;
 RA Noguuchi M., Nakamura Y., Russell S.M., Ziegler S.F., Tsang M., Cao X.,
 RA Leonard W.J.;
 RT "interleukin-2 receptor gamma chain: a functional component of the
 RT interleukin-7 receptor";
 RL Science 262:1877-1880(1993).
 RN [7]
 RP 3D-STRUCTURE MODELING OF 57-248.
 RX MEDLINE=95111955; PubMed=7529123;
 RA Bamorough P., Hedgecock C.J., Richards W.G.;
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular
 RT modelling";
 RL Structure 2:839-851(1994).
 RN [8]
 RP VARIANT XSCID PHE-115; CYS-240 AND ILE-241.
 RX MEDLINE=94130970; PubMed=829698;
 RA Disanto J.P., Dautry-Varsat A., Certain S., Fischer A.,
 RA de Saint Basile G.;
 RT "interleukin-2 (IL-2) receptor gamma chain mutations in X-linked
 RT severe combined immunodeficiency disease result in the loss of
 RT high-affinity IL-2 receptor binding";
 RL Eur. J. Immunol. 24:475-479(1994).
 RN [9]
 RP VARIANT XSCID LYS-68.
 RX MEDLINE=94375038; PubMed=8088810;
 RA Markiewicz S., Subtil A., Dautry-Varsat A., Fischer A.,
 RA de Saint Basile G.;
 RT "Detection of three nonsense mutations and one missense mutation in
 RT the interleukin-2 receptor gamma chain gene in SCIDX1 that
 RT differentially affect the mRNA processing";
 RL Genomics 21:291-293(1994).
 RN [10]
 RP VARIANT XSCID HIS-162.
 RX MEDLINE=94300093; PubMed=8027558;
 RA Ishii N., Asao H., Kimura Y., Takeshita T., Nakamura M., Tsuchiya S.,
 RA Kono T., Maeda M., Uchiyama T., Sugamura K.;
 RT "Impairment of ligand binding and growth signaling of mutant IL-2
 RT receptor gamma-chains in patients with X-linked severe combined
 RT immunodeficiency";
 RL J. Immunol. 153:1310-1317(1994).
 RN [11]
 RP VARIANT XSCID ASN-39.
 RX MEDLINE=95023932; PubMed=7937790;
 RA Disanto J.P., Rieux-Laucat F., Dautry-Varsat A., Fischer A.,
 RA de Saint Basile G.;
 RT "Defective human interleukin 2 receptor gamma chain in an atypical X
 RT chromosome-linked severe combined immunodeficiency with peripheral T
 RT cells";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9466-9470(1994).
 RN [12]
 RP VARIANT XSCID CYS-226 AND HIS-226.
 RX MEDLINE=95397841; PubMed=7688284;
 RA Pepper A.E., Buckley R.H., Small T.N., Puck J.M.;
 RT "Two mutational hotspots in the interleukin-2 receptor gamma chain
 RT gene causing human X-linked severe combined immunodeficiency";
 RL Am. J. Hum. Genet. 57:564-571(1995).
 RN [13]
 RP VARIANT XSCID SER-183.
 RX MEDLINE=96013903; PubMed=7557965;
 RA Clark P.A., Lester T., Genet S., Jones A.M., Hendriks R.,
 RA Levisky R.L., Kinon C.;
 RT "Screening for mutations causing X-linked severe combined
 RT immunodeficiency in the IL-2R gamma chain gene by single-strand
 RT conformation polymorphism analysis";
 RL Hum. Genet. 96:427-432(1995).
 RN [14]
 RP VARIANT XSCID GLN-237 G-H-W INS.
 RX MEDLINE=95164726; PubMed=7860773;
 RA Puck J.M., Pepper A.E., Bedard P.-M., Laframboise R.;
 RT "Female germ line mosaicism as the origin of a unique IL-2 receptor
 RT gamma-chain mutation causing X-linked severe combined
 RT immunodeficiency";
 RL J. Clin. Invest. 95:895-899(1995).

RN [15]
 RP VARIANT XSCID GLN-293.
 RX MEDLINE=95190013; PubMed=7883965;
 RA Schmeistleg F.C., Leonard W.J., Noguuchi M., Berg M., Rudloff H.E.,
 RA Denney R.M., Dave S.K., Brooks E.G., Goldman A.S.;
 RT "Missense mutation in exon 7 of the common gamma chain causes a
 RT moderate form of X-linked combined immunodeficiency";
 RL J. Clin. Invest. 95:1169-1173(1995).
 RN [16]
 RP VARIANT XSCID ARG-115.
 RX MEDLINE=97042245; PubMed=8900089;
 RA Stephan V., Mann V., Le Deist F., Dirksen U., Broecker B.,
 RA Mueller-Fleckenstein I., Horneff G., Schroten H., Fischer A.,
 RA de Saint Basile G.;
 RT "Atypical X-linked severe combined immunodeficiency due to possible
 RT spontaneous reversion of the genetic defect in T cells";
 RL New Engl. J. Med. 335:1563-1567(1996).
 RN [17]
 RP VARIANT XSCID GLN-285.
 RX MEDLINE=97295088; PubMed=9150740;
 RA Jones A.M., Clark P.A., Katz F., Genet S., McMahon C., Alterman L.,
 RA Cant A., Kinon C.;
 RT "B-cell-negative severe combined immunodeficiency associated with a
 RT common gamma chain mutation";
 RL Hum. Genet. 99:677-680(1997).
 RN [18]
 RP VARIANT XSCID CYS-222.
 RX MEDLINE=98064061; PubMed=9399950;
 RA Sharfe N., Shahar M., Rolifman C.M.;
 RT "An interleukin-2 receptor gamma chain mutation with normal thymus
 RT morphology";
 RL J. Clin. Invest. 100:3036-3043(1997).
 CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
 CC INTERLEUKINS.
 CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
 CC PROBABLY ALSO THE IL-13 RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A SEVERE COMBINED
 CC IMMUNODEFICIENCY, WHICH IS KNOWN AS AGAMMAGLOBULINEMIA, SWISS TYPE
 CC OR X-LINKED SEVERE COMBINED IMMUNODEFICIENCY DISEASE (XSCID).
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC -1- DATABASE: NAME=PRO; NOTE=CD guide c0132 entry.
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd132.htm".
 CC -1- DATABASE: NAME=IL2RGbase; NOTE=X-linked SCID mutation database;
 CC WWW="http://www.nigrl.nih.gov/DIR/GMB/SCID/".
 CC -----
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 CC -----
 DR EMBL: D11086; BAA01857.1; -;
 DR EMBL: L12183; AAA59145.1; -;
 DR EMBL: L12178; AAA58145.1; JOINED.
 DR EMBL: L12176; AAA59145.1; JOINED.
 DR EMBL: L12177; AAA59145.1; JOINED.
 DR EMBL: L12179; AAA59145.1; JOINED.
 DR EMBL: L12180; AAA59145.1; JOINED.
 DR EMBL: L12181; AAA59145.1; JOINED.
 DR EMBL: L12182; AAA59145.1; JOINED.
 DR EMBL: L19546; AAC37524.1; -;
 DR PIR: A42565; A42565.
 DR PDB: 1ILM; 26-JAN-95.
 DR PDB: 1ILN; 26-JAN-95.
 DR MIM: 308380; -;
 DR MIM: 300400; -;
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.

Query Match 100.0%; Score 1288; DB 1; Length 369;
 Best Local Similarity 100.0%; Pred. No. 9,9e-102; Mismatches 0; Indels 0; Gaps 0;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTITPNGNEDTADFLTPTDLSVSTPLPEVOCFVFNVEYMNCTNNSSEPOP 60
 |||||||
 DB 23 LNTTITPNGNEDTADFLTPTDLSVSTPLPEVOCFVFNVEYMNCTNNSSEPOP 82
 |||||||

QY 61 TNLTLHWKNSNDKVKQCSHYLFSEETISGCOLKKEIHLVOTFVVOLODPREPRROA 120
 |||||||
 DB 83 TNLTLHWKNSNDKVKQCSHYLFSEETISGCOLKKEIHLVOTFVVOLODPREPRROA 142
 |||||||

QY 121 TOMLKQNLVTPWAPENLTILHKLSESOLELNNNREFLNHLEHLVQYRTDMDHSWTEQSV 180
 |||||||
 DB 143 TOMLKQNLVTPWAPENLTILHKLSESOLELNNNREFLNHLEHLVQYRTDMDHSWTEQSV 202
 |||||||

QY 181 DYRKRFSLPSVDGOKRTYFRVRSRFPNPLCGSAQHWSEMSHPRIHMGSTNSKEN 232
 |||||||
 203 DYRKRFSLPSVDGOKRTYFRVRSRFPNPLCGSAQHWSEMSHPRIHMGSTNSKEN 254
 |||||||

RESULT 2
 CYRG_CANFA STANDARD; PRT; 373 AA.

ID CYRG_CANFA P40321:
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Cytokine receptor common gamma chain precursor (Gamma-C)
 DE (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
 GN IL2RG.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Spleen;
 RX MEDLINE=95130114; PubMed=7829104;
 RA Henthorn P.S., Sömberg R.L., Fimiani V.M., Puck J.M., Patterson D.F.,
 RA Felsburg P.J.;
 RT "IL-2R gamma gene microdeletion demonstrates that canine X-linked
 RT severe combined immunodeficiency is a homologue of the human
 RT disease.";
 RL Genomics 23:69-74(1994).
 CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
 CC INTERLEUKINS.
 CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
 CC PROBABLY ALSO THE IL-13 RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A CANINE X-LINKED
 CC SEVERE COMBINED IMMUNODEFICIENCY.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC
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 CC
 CC EMBL; U04361; AAC48403.1; -
 DR HSSP; P31785; IILN.
 DR InterPro; IPR002996; CRIA.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003531; Hematopo_receptor_S_F1.
 DR Pfam; PF00041; fn3; 1.
 DR SMART; SM00060; FN3; 1.
 DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 22
 FT CHAIN 23 373
 FT DOMAIN 23 261
 FT TRANSMEM 262 283
 FT DOMAIN 284 373
 FT DOMAIN 151 249
 FT DISULFID 62 72
 FT DISULFID 102 115
 FT CARBOHYD 24 24
 FT CARBOHYD 71 71
 FT CARBOHYD 75 75
 FT CARBOHYD 84 84
 FT CARBOHYD 159 159
 FT CARBOHYD 164 164
 FT CARBOHYD 249 249
 SQ SEQUENCE 373 AA; 42516 MW; 03A0DELFB089DB8 CRC64;

Query Match 85.2%; Score 1097; DB 1; Length 373;
 Best Local Similarity 82.8%; Pred. No. 1.3e-85; Mismatches 16; Indels 0; Gaps 0;
 Matches 192; Conservative 24; Mismatches 16; Indels 0; Gaps 0;

QY 1 LNTTITPNGNEDTADFLTPTDLSVSTPLPEVOCFVFNVEYMNCTNNSSEPOP 60
 ||:|||||
 DB 23 LNSTVPMPNGNEDITPDPFLATPSETLSVSLPLPEVOCFVFNVEYMNCTNNSSEPOP 82
 |||||||

QY 61 TNLTLHWKNSNDKVKQCSHYLFSEETISGCOLKKEIHLVOTFVVOLODPREPRROA 120
 |||||||

DB 83 TNLTLHWKNSNDKVKQCSHYLFSEETISGCOLKKEIHLVOTFVVOLODPREPRROA 142
 |||||||

QY 121 TOMLKQNLVTPWAPENLTILHKLSESOLELNNNREFLNHLEHLVQYRTDMDHSWTEQSV 180
 |||||||

DB 143 TOMLKQNLVTPWAPENLTILHKLSESOLELNNNREFLNHLEHLVQYRTDMDHSWTEQSV 202
 |||||||

QY 181 DYRKRFSLPSVDGOKRTYFRVRSRFPNPLCGSAQHWSEMSHPRIHMGSTNSKEN 232
 ||:|||||

DB 203 DYRKRFSLPSVDGOKRTYFRVRSRFPNPLCGSAQHWSEMSHPRIHMGSTNSKEN 254
 |||||||

RESULT 3
 CYRG_BOVIN STANDARD; PRT; 379 AA.

ID CYRG_BOVIN Q95118:
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Cytokine receptor common gamma chain precursor (Gamma-C)
 DE (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
 GN IL2RG.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96268473; PubMed=8672241;
 RA Yoo J., Stone R.T., Solinas-Pardo S., Fries R., Beattie C.W.;
 RT "Cloning and chromosomal mapping of bovine interleukin-2 receptor
 RT gamma gene.";
 RL DNA Cell Biol. 15:453-459(1996).
 CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
 CC INTERLEUKINS.
 CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
 CC PROBABLY ALSO THE IL-13 RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC
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 DR EMBL: U33748; AAB07812.1; -
 DR HSSP: P31785; IILN.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003531; Hematopo_receptor_S_Fl.
 DR Pfam: PF00041; fn3; 1.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01355; Hematopo_REC_S_Fl; 1.
 DR PROSITE: Transmembrane; Glycoprotein; Signal.
 KM Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 379
 FT DOMAIN 23 269
 FT TRANSMEM 270 290
 FT DOMAIN 291 379
 FT DOMAIN 158 256
 FT DISULFID 68 78
 FT DISULFID 109 122
 FT CARBOHYD 77 77
 FT CARBOHYD 81 81
 FT CARBOHYD 90 90
 FT CARBOHYD 166 166
 FT CARBOHYD 171 171
 SQ SEQUENCE 379 AA: 43037 MW: 336FAD9C9B032178 CRC64;
 Query Match 76.98; Score 990.5; DB 1; Length 379;
 Best Local Similarity 76.2%; Pred. No. 1.4e-76;
 Matches 182; Conservative 21; Mismatches 29; Indels 7; Gaps 2;
 QY 1 LNTTILPAGNED-----TTAEFLTPPTDLSYSTLPLEVOCFVFNVMCTNNS 54
 Db 23 LNPKEFLPSNEDIGKPGTGSDFILSTPAGLVDSTLPKVCQCFVFNVMCTNNS 82
 QY 55 GSEPOPNLTLHYWKYK-SDNKVKQKSHYLSSEETSCQLOKKEIHYQFFVQLODP 113
 Db 83 SSEEQPNLTLHYGRNFGNDKLCQGHYLFSEGITSGCWGKKEIRLYETFFVQLODP 142
 QY 114 REPRRQTMALKTQNTVTPAPENLTILHKLESQELMNNRNINCEHLVQYFQMDH 173
 Db 143 REHKQKQKMLKLDVLPAPENLTILRNSEHQLELSMKNYLDHCLHLVQYSDNR 202
 QY 174 SMTBQSYDVYHAKFSLPSVDGQKRYTFRVSRNPCLCGAQHMSHNPILHMSNTSKEN 232
 Db 203 SMTBQSYDVYHAKFSLPSVDGQKRYTFRVSRNPCLCGAQHMSHNPILHMSNTSKEN 261
 RESULT 4
 CYRG_MOUSE STANDARD; PRT; 369 AA.
 ID CYRG_MOUSE
 AC P34902;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Cytokine receptor common gamma chain precursor (Gamma-C)
 DE (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
 GN IL2RG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93277575; PubMed=8503926;
 RA Kunita S., Kondo M., Takeshita T., Asao H., Nakamura M., Sugamura K.,
 RT "Cloning of the mouse interleukin 2 receptor gamma chain:
 RT demonstration of functional differences between the mouse and human
 RT receptors.";
 RL Blochem. Biophys. Res. Commun. 193:356-363(1993).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=CBA/CA;
 RX MEDLINE=93391374; PubMed=8378320;
 RX Cao X., Kozak C.A., Liu Y.J., Noguchi M., O'Connell E., Leonard W.J.;
 RT "Characterization of cDNAs encoding the murine interleukin 2 receptor
 RT (IL-2R) gamma chain: chromosomal mapping and tissue specificity of
 RT IL-2R gamma chain expression.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468(1993).
 RP [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9336191; PubMed=8359699;
 RA Kobayashi N., Nakagawa S., Minami Y., Taniguchi T., Kono T.;
 RT "Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor
 RT gamma.";
 RL Gene 130:303-304(1993).
 RP [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95104285; PubMed=7805729;
 RA Disanto J.P., Certain S., Wilson A., Macdonald H.R., Avner P.,
 RA Fischer A., de Saint Basile G.;
 RT "The murine interleukin-2 receptor gamma chain gene: organization,
 RT chromosomal localization and expression in the adult thymus.";
 RL Eur. J. Immunol. 24:3014-3018(1994).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6.S;
 RX MEDLINE=96341745; PubMed=8750189;
 RX Chiu R.K., Droll A., Cooper D.L., Dougherty S.T., Dirks J.F.,
 RA Dougherty G.J.;
 RT "Molecular mechanisms regulating the hyaluronan binding activity of
 RT the adhesion protein CD44.";
 RL J. Neurooncol. 26:231-239(1995).
 CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
 CC INTERLEUKINS.
 CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
 CC -1- PROBABLY ALSO THE IL-13 RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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 DR EMBL: D13821; BAA02974.1; -
 DR EMBL: U21795; AAA64279.1; -
 DR EMBL: D13565; BAA02760.1; -
 DR EMBL: L20048; AAA39286.1; -
 DR EMBL: S75852; AAB32904.1; -
 DR EMBL: S75844; AAB32904.1; JOINED.
 DR EMBL: S75845; AAB32904.1; JOINED.
 DR EMBL: S75847; AAB32904.1; JOINED.
 DR EMBL: S75848; AAB32904.1; JOINED.
 DR EMBL: S75849; AAB32904.1; JOINED.
 DR EMBL: S75850; AAB32904.1; JOINED.
 DR EMBL: S75851; AAB32904.1; JOINED.
 DR EMBL: X75337; CAA53085.1; -
 DR PIR: JN0592; JN0592.
 DR PIR: JN0775; JN0775.
 DR HSSP: P31785; IILN.
 DR MGD: MGI:96551; IL2rg.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003531; Hematopo_receptor_S_Fl.
 DR Pfam: PF00041; fn3; 1.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01355; Hematopo_REC_S_Fl; 1.
 KM Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 22
 FT BY SIMILARITY.

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FT CHAIN 23 369 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT DOMAIN 23 263 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 264 284 POTENTIAL.
FT DOMAIN 285 369 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 151 250 FIBRONECTIN TYPE-III.
FT DISULFID 62 72 POTENTIAL.
FT CARBOHYD 102 115 POTENTIAL.
FT CARBOHYD 71 71 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 96 96 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAc. . .) (POTENTIAL).
SQ SEQUENCE 369 AA; 42241 MW; CB25AB459077AC7 CRC64;

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Query Match 66.3%; Score 853.5; DB 1; Length 369;
Best local similarity 67.2%; Pred. No. 4,9e-65;
Matches 156; Conservative 33; Mismatches 42; Indels 1; Gaps 1;

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2 NTFILTPNGEDTADPEFLTPMPDLSVSTPLPEVOCFVFNRYMCTMNSSEPOPT 61
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Db 24 SSVLMSSANEDIKADLITSTAPEHLSATPLPEVOCFVFNRYMCTMNSSEPOAT 83
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 62 NLTLYWTKNSDNKVKQCSHYLFSEETISGCOLQKEHLHYQTFVVOLODPREPRQAT 121
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 84 NLTLYWTKNSDNKVKQCSHYLFSEETISGCOLQKEHLHYQTFVVOLODPREPRQAV 143
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 122 QMLKLONLVTPWAPENLTPLKLSQSLQELMNMNRP--NHCLHLYQVFTDMDHSWT 180
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 144 OKLNTLONLVTPWAPENLTPLKLSQSLQELMNMNRP--NHCLHLYQVFTDMDHSWT 203
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 181 DYNHRSKLSVSDGOKRYEVRFRSRFNPFLGSAQHSEMSHPFHMSGNSNTSKEN 232
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 204 NHPRRSLSVSDGOKRYEVRFRSRFNPFLGSAQHSEMSHPFHMSGNSNTSKEN 255
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 5
ID 1132_HUMAN STANDARD: PRT; 380 AA.
AC 014627; 000667;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-13 receptor alpha-2 chain precursor (Interleukin-13
  binding protein).
GN IL13RA2 OR IL13R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Renal cell carcinoma;
RX MEDLINE=96279273; PubMed=8663118;
RA Caput D., Laurent P., Kagnad M., Lelias J.M., Lefort S., Vta N.,
  Ferrara P.;
RT "Cloning and characterization of a specific interleukin (IL)-13
  binding protein structurally related to the IL-5 receptor alpha
  chain."
RL J. Biol. Chem. 271:16921-16926(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Donaldson D.D., Whiters M.J., Fitz L., Neben T., Flinnerty H.,
  Henderson S.L., O'Hara R.M., Jr., Turner K.J., Wood C.R., Collins M.;
  Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97321053; PubMed=9177784;
RA Guo J., Aptou F., Meilert H.P., Lebeau B., Jacques Y., Minvielle S.;
  Chromosome mapping and expression of the human Interleukin-13

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RT receptor."
RL Genomics 42:141-145(1997).
CC -1- FUNCTION: BINDS AS A MONOMER WITH HIGH AFFINITY TO INTERLEUKIN-13
  (IL-13), BUT NOT TO IL-4.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
CC This SWISS-Prot entry is copyright. It is produced through a collaboration
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X95302; CA64617.1; -
DR EMBL; U70981; AAB17170.1; -
DR EMBL; Y08768; CA70021.1; -
DR MM; 300130; -
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003661; FN_III.
DR InterPro; IPR003632; Hematopo_receptor_S_F2.
DR Pfam; PF00041; fn3.1.
DR PROSITE; PS0156; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 380 INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN.
FT DOMAIN 27 343 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 344 363 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 364 380 BY SIMILARITY.
FT DISULFID 145 155 BY SIMILARITY.
FT DISULFID 184 197 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 115 115 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 215 215 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAc. . .) (POTENTIAL).
SQ SEQUENCE 380 AA; 44176 MW; 3C6ACB1B5562C887 CRC64;

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Query Match 16.1%; Score 207; DB 1; Length 380;
Best local similarity 25.4%; Pred. No. 2e-10;
Matches 60; Conservative 46; Mismatches 106; Indels 24; Gaps 9;

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OY 9 NCMEDTADPEFLTPMPDLSVSTPLPEVOCFVFNRYMCTMNSSEPOPT-----T 61
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 NGSE-VQSSMATTYTWISPOGIPETKYQDMCYVYIMQYLCSW-----KPGIVLDT 167
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 62 NLTLYWTKNSDNKVKQCSHYLFSEETISGCOLQKEHLHYQTFVVOLODPRE--PRQ 119
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 168 NYNLFYWEGLDH--ALQCVYIKADQNGICRFYLEASDKRDFYICVNGSSENKPIRS 225
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 120 AQMLKLONLVTPWAPENLTPLKLSQSLQELMNMN--NRLNHCLHLYQVFTDMDHSWT 176
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 226 SYTFQQLQIVKFLPPYVLPPTRESCEIKLWSIPLGIPACRDYDIEIRED-DITLV 284
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 177 EOSVDYRHKFSVSDGOKRYEVRFRSRFNPFLGSAQHSEMSHPFHMSGNSNTSKEN 231
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 285 TATVE-NETIYIKTINERQLCFVRSKVIYICSDGIMSEMSKQCKWEGEDLSK 339
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 6
ID 1131_MOUSE STANDARD: PRT; 424 AA.
AC 009030;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-
  13RA-1) (Interleukin-13 binding protein) (NR4).
GN IL13RA1 OR IL13R OR IL13R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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DR EMBL: U81379; AAD00510.3; -
 DR HSSP: P40189; IBCU.
 DR MIM: 300119; -
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR003532; Hematopo_receptor_S_F2.
 DR Pfam: PF00041; fn3; 1.
 DR PROSITE: PS01356; HEMATOPO_REC_S_F2; 1.
 DR Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 427 INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN.
 FT DOMAIN 22 343 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 344 367 POTENTIAL.
 FT DOMAIN 368 427 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 39 102 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 46 95 POTENTIAL.
 FT DISULFID 134 144 BY SIMILARITY.
 FT DISULFID 173 185 BY SIMILARITY.
 FT CARBOHYD 37 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 130 130 T -> I (IN REF. 3).
 FT CONFLICT 358 358 G -> D (IN REF. 3).
 SQ SEQUENCE 427 AA; 48759 MW; 5983B3B8F54107B CRC64;

Query Match 13.8%; Score 178; DB 1; Length 427;
 Best Local Similarity 26.7%; Pred. No. 6.4e-08;
 Matches 58; Conservative 38; Mismatches 83; Indels 38; Gaps 11;

OY 37 EVQCFVNEVYKNTWSSSEPPQ-TNLTLYHYKNSDNDKVKCSHYLFSEETISGC-- 93
 DB 131 ELQCIIMHNSLYKMSGSMWLPGRNTPPTNTLYLVYHRSLS-EKIHQEN-IPREGQYFGGSF 187
 OY 94 QLOKKEIHLYQTFVYQLO--QDRPRROATOMKLONTLVIPWAPN-ENULTLHKLSQLE 149
 DB 188 DLTLYKDSSEFQSHVOIWKKNAGKIKPSFNIVPLTSHVKDDPRPIKMSFH--NDL 244
 OY 150 LNMNN--RELINCHLEHLVQYRTMDHNSWT-----DQSDYRHKESLP 189
 DB 245 VQMEHPQNFISKCL----FYEYEVNNSQTEHNHVFYVOEAKCENPEFERVENTISCEWVP 300
 DB 301 GVLPTLMTVTRIRVKTNKLCTYEDDKLMSNWGSEMSIG 337
 RESULT 8
 CYRB_HUMAN STANDARD; PRT; 897 AA.
 ID CYRB_HUMAN P32927;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cytokine receptor common beta chain precursor (CDW131 antigen).
 GN CSF2RB OR IL3RB OR IL3RB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91088571; PubMed=1702217;
 RA Hayashida K., Kitamura T., Gorman D.M., Arai K., Yokota T.,
 Miyajima A.;
 RT Molecular cloning of a second subunit of the receptor for human

RT granulocyte-macrophage colony-stimulating factor (GM-CSF);
 RT reconstitution of a high-affinity GM-CSF receptor";
 RT Proc. Natl. Acad. Sci. U.S.A. 87:9655-9659(1990).
 RN [2]
 RP REVISION TO 454.
 RA Kitamura T.;
 RL Submitted (FEB-1991) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5
 CC AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
 CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide cdw131 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw131.htm".
 CC -----
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 CC or send an email to license@isb-sdb.ch).
 CC -----
 CC EMBL: M59941; AAA18171.1; -
 CC PIR: A39255; A39255.
 CC HSSP: P19235; 1EBA.
 DR MIM: 138981; -
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR000282; Cytok_receptor_2.
 DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 2.
 DR PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
 DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
 KW SIGNAL 1 16
 FT CHAIN 17 897 CYTOKINE RECEPTOR COMMON BETA CHAIN.
 FT DOMAIN 17 443 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 444 460 POTENTIAL.
 FT DOMAIN 461 897 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 129 238 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 336 434 FIBRONECTIN TYPE-III 2.
 FT DISULFID 35 45 BY SIMILARITY.
 FT DISULFID 75 91 BY SIMILARITY.
 FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 346 346 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 897 AA; 97335 MW; 3398E37FDB8F393A CRC64;

Query Match 12.3%; Score 159; DB 1; Length 897;
 Best Local Similarity 26.4%; Pred. No. 6.4e-06;
 Matches 55; Conservative 40; Mismatches 79; Indels 34; Gaps 12;

OY 38 VOCFVNEVYKNTWSSSEPPQTNLTLYHYKNSDNDKVKCSHYLFSEETISGC 93
 DB 248 LECFDDAAVLSGSEWYRKE-VASSVSFGLFKPSDPAGAGEECSPLYRDEGLSHRRHC 306
 OY 94 QLOKKEIHLYQTFVYQLODRPRROATOMKLONTLVIPWAPNLTLHKLSQLELANN 153
 DB 307 QIIPDPATGQYIVSYQ---PRR-AEKIK-SVNIQWAPSLVNTKGDG-YSLRME 359
 OY 154 NRELINCHLEHL-----VQYRTD---WDHSWTESVDYRHKESLPVQDGKRYTFRRSR 204
 DB 360 TMRKRY--EHIDHTEFLQYRKDTATWDSKTE-TLQAHSMALPALEPSTRYWARVRRT 416
 OY 205 ----FNPLCSAQHSEMSHPHMGNT 228
 DB 417 SRIGYNGI-----WSEMSRARSMDTES 438

Query Match	Best Local Similarity	Score	DB 1	Length	DB 2	DB 3	DB 4	DB 5	DB 6	DB 7	DB 8	DB 9	DB 10	DB 11	DB 12	DB 13	DB 14	DB 15	DB 16	DB 17	DB 18	DB 19	DB 20	DB 21	DB 22	DB 23	DB 24	DB 25	DB 26	DB 27	DB 28	DB 29	DB 30	DB 31	DB 32	DB 33	DB 34	DB 35	DB 36	DB 37	DB 38	DB 39	DB 40	DB 41	DB 42	DB 43	DB 44	DB 45	DB 46	DB 47	DB 48	DB 49	DB 50	DB 51	DB 52	DB 53	DB 54	DB 55	DB 56	DB 57	DB 58	DB 59	DB 60	DB 61	DB 62	DB 63	DB 64	DB 65	DB 66	DB 67	DB 68	DB 69	DB 70	DB 71	DB 72	DB 73	DB 74	DB 75	DB 76	DB 77	DB 78	DB 79	DB 80	DB 81	DB 82	DB 83	DB 84	DB 85	DB 86	DB 87	DB 88	DB 89	DB 90	DB 91	DB 92	DB 93	DB 94	DB 95	DB 96	DB 97	DB 98	DB 99	DB 100	DB 101	DB 102	DB 103	DB 104	DB 105	DB 106	DB 107	DB 108	DB 109	DB 110	DB 111	DB 112	DB 113	DB 114	DB 115	DB 116	DB 117	DB 118	DB 119	DB 120	DB 121	DB 122	DB 123	DB 124	DB 125	DB 126	DB 127	DB 128	DB 129	DB 130	DB 131	DB 132	DB 133	DB 134	DB 135	DB 136	DB 137	DB 138	DB 139	DB 140	DB 141	DB 142	DB 143	DB 144	DB 145	DB 146	DB 147	DB 148	DB 149	DB 150	DB 151	DB 152	DB 153	DB 154	DB 155	DB 156	DB 157	DB 158	DB 159	DB 160	DB 161	DB 162	DB 163	DB 164	DB 165	DB 166	DB 167	DB 168	DB 169	DB 170	DB 171	DB 172	DB 173	DB 174	DB 175	DB 176	DB 177	DB 178	DB 179	DB 180	DB 181	DB 182	DB 183	DB 184	DB 185	DB 186	DB 187	DB 188	DB 189	DB 190	DB 191	DB 192	DB 193	DB 194	DB 195	DB 196	DB 197	DB 198	DB 199	DB 200	DB 201	DB 202	DB 203	DB 204	DB 205	DB 206	DB 207	DB 208	DB 209	DB 210	DB 211	DB 212	DB 213	DB 214	DB 215	DB 216	DB 217	DB 218	DB 219	DB 220	DB 221	DB 222	DB 223	DB 224	DB 225	DB 226	DB 227	DB 228	DB 229	DB 230	DB 231	DB 232	DB 233	DB 234	DB 235	DB 236	DB 237	DB 238	DB 239	DB 240	DB 241	DB 242	DB 243	DB 244	DB 245	DB 246	DB 247	DB 248	DB 249	DB 250	DB 251	DB 252	DB 253	DB 254	DB 255	DB 256	DB 257	DB 258	DB 259	DB 260	DB 261	DB 262	DB 263	DB 264	DB 265	DB 266	DB 267	DB 268	DB 269	DB 270	DB 271	DB 272	DB 273	DB 274	DB 275	DB 276	DB 277	DB 278	DB 279	DB 280	DB 281	DB 282	DB 283	DB 284	DB 285	DB 286	DB 287	DB 288	DB 289	DB 290	DB 291	DB 292	DB 293	DB 294	DB 295	DB 296	DB 297	DB 298	DB 299	DB 300	DB 301	DB 302	DB 303	DB 304	DB 305	DB 306	DB 307	DB 308	DB 309	DB 310	DB 311	DB 312	DB 313	DB 314	DB 315	DB 316	DB 317	DB 318	DB 319	DB 320	DB 321	DB 322	DB 323	DB 324	DB 325	DB 326	DB 327	DB 328	DB 329	DB 330	DB 331	DB 332	DB 333	DB 334	DB 335	DB 336	DB 337	DB 338	DB 339	DB 340	DB 341	DB 342	DB 343	DB 344	DB 345	DB 346	DB 347	DB 348	DB 349	DB 350	DB 351	DB 352	DB 353	DB 354	DB 355	DB 356	DB 357	DB 358	DB 359	DB 360	DB 361	DB 362	DB 363	DB 364	DB 365	DB 366	DB 367	DB 368	DB 369	DB 370	DB 371	DB 372	DB 373	DB 374	DB 375	DB 376	DB 377	DB 378	DB 379	DB 380	DB 381	DB 382	DB 383	DB 384	DB 385	DB 386	DB 387	DB 388	DB 389	DB 390	DB 391	DB 392	DB 393	DB 394	DB 395	DB 396	DB 397	DB 398	DB 399	DB 400	DB 401	DB 402	DB 403	DB 404	DB 405	DB 406	DB 407	DB 408	DB 409	DB 410	DB 411	DB 412	DB 413	DB 414	DB 415	DB 416	DB
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OY		38	VOCFFENFVWNNKJMNSSSE--PQPTNLTHLHWKNSNDKOKCSHSLFSPETISG---C	93
Dd		34	IRCSLSLEKETSCWMKPESDGGTLTNTLT--FYSKDSEELIECPDYR-----TSGN	86
OY		94	OLQKKELHLVOTFVVVLODDPREPRQAT--OMELKIQLNVLTPWADENLTJLH-KUSEOLET	150
Dd		87	YFNKKHTSPMTFTNFITVATNEIGSNSSDPYVDVTSTIVPGSVANTLTLETKRANIMYL	146
OY		151	--NNNNRLL-----NHCLLEHLVQVTRTMDHSWTQSVDYRHKEFLPSVDQGKRTFPVR	203
Dd		147	WAKMSPELLDAASSHHLYHYELRLKPEKEEMETTISVGVOYOCKINRLNMGMRIVVOYRC	206
OY		204	RFNPLCGSAQHMSWSNPDIH 223	
Dd		207	TLDP-----GEWSEWSSERH 221	
RESULT		10		
ID	GMCRR_HUMAN	STANDARD:	PRT; 400 AA.	
AC	P15509; Q14429; Q14430; Q14431; O00207; Q16564;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Granulocyte-macrophage colony-stimulating factor receptor alpha chain precursor (GM-CSF-R-alpha) (GMR) (CDW116) (CD116 antigen).			
GN	(CSF2RA OR CSF2RA OR CSF2RA OR CSF2RX) AND (CSF2RAY OR CSF2RA OR CSF2R OR CSF2RY).			
OS	Homo sapiens (Human).			
OC	Euryarchaeota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	MCB1_TaxID=9606;			
NN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Placenta;			
RC	MEDLINE=90059966; PubMed=2555171;			
RA	Gearing D.P., King J.A., Gough N.M., Nicola N.A.;			
RT	"Expression cloning of a receptor for human granulocyte-macrophage colony-stimulating factor."			
RL	EMBO J. 8:3667-3676(1989).			
NN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	MEDLINE=94193800; PubMed=8144676;			
RA	Nakagawa Y., Kosugi H., Miyajima A., Arai K.I., Yokota T.;			
RT	"Structure of the gene encoding the alpha subunit of the human granulocyte-macrophage colony stimulating factor receptor."			
RT	Implications for the evolution of the cytokine receptor superfamily."			
RL	J. Biol. Chem. 269:10905-10912(1994).			
NN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	MEDLINE=91352066; PubMed=1715577;			
RA	Crosier R.E., Wong G.G., Mathey-Prevot B., Nathan D.G., Sleff C.A.;			
RT	"A functional isoform of the human granulocyte/macrophage colony-stimulating factor receptor has an unusual cytoplasmic domain."			
RL	Proc. Natl. Acad. Sci. U.S.A. 88:7744-7748(1991).			
NN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 3).			
RC	TISSUE=Placenta;			
RC	MEDLINE=91088339; PubMed=2148207;			
RA	Ashworth A., Kraft A.;			
RT	"Cloning of a potentially soluble receptor for human GM-CSF."			
RL	Nucleic Acids Res. 18:7176-7178(1990).			
NN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM 3).			
RC	MEDLINE=91376112; PubMed=1832774;			
RA	Raines M.A., Liu L., Quan S.G., Joe V., Dipersio J.F., Golde D.W.;			
RT	"Identification and molecular cloning of a soluble human granulocyte-macrophage colony-stimulating factor receptor."			
RL	Proc. Natl. Acad. Sci. U.S.A. 88:8203-8207(1991).			
NN	[6]			
RP	SEQUENCE FROM N.A. (ISOFORMS 4 AND 5).			
RC	TISSUE=Blood;			

RX MEDLINE=94368898; PubMed=8086503;
 RA Hu X., Emanuel P.D., Zuckerman K.S.;
 RT "Cloning and sequencing of the cDNA encoding two alternative
 RT splicing-derived variants of the alpha subunit of the granulocyte-
 RT macrophage colony-stimulating factor receptor.";
 RL Blochim. Biophys. Acta 1223:306-308(1994).
 RN [7].
 RP SEQUENCE FROM N.A. (ISOFORM 6).
 RA Hu X., Zuckerman K.S.;
 RT "Cloning and sequencing of the cDNA variant with 397 bp missing
 RT for the GM-CSF receptor alpha subunit.";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR FOR GRANULOCYTE-MACROPHAGE COLONY-
 CC STIMULATING FACTOR. TRANSDUCES A SIGNAL THAT RESULTS IN THE
 CC PROLIFERATION, DIFFERENTIATION, AND FUNCTIONAL ACTIVATION OF
 CC HEMATOPOIETIC CELLS.
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
 CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ISOFORMS 3, 4 AND 6
 CC ARE PROBABLY SOLUBLE.
 CC -1- ALTERNATIVE PRODUCTS: 6 ISOFORMS; 1 (SHOWN HERE), 2, 3, 4, 5 AND
 CC 6: ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC -----
 DR EMBL: X17648; CA55638.1; -;
 DR EMBL: D26628; BAA05656.1; -;
 DR EMBL: D26618; BAA05656.1; JOINED.
 DR EMBL: D26619; BAA05656.1; JOINED.
 DR EMBL: D26620; BAA05656.1; JOINED.
 DR EMBL: D26621; BAA05656.1; JOINED.
 DR EMBL: D26622; BAA05656.1; JOINED.
 DR EMBL: D26623; BAA05656.1; JOINED.
 DR EMBL: D26624; BAA05656.1; JOINED.
 DR EMBL: D26625; BAA05656.1; JOINED.
 DR EMBL: D26626; BAA05656.1; JOINED.
 DR EMBL: D26627; BAA05656.1; JOINED.
 DR EMBL: M64445; AAA35908.1; -;
 DR EMBL: X54935; CA53697.1; -;
 DR EMBL: M73832; AAA35909.1; -;
 DR EMBL: L29348; AAA60961.1; -;
 DR EMBL: L29349; AAA60962.1; -;
 DR EMBL: U93096; AAB51535.1; -;
 DR PIR: S06945; S06945.
 DR MIM: 306250; -;
 DR MIM: 425000; -;
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003532; Hematopo_receptor_S_F2.
 DR PROSITE: PS01356; Hematopo_REC_S_F2; 1.
 KW Receptor; Transmembrane; Glycoprotein; signal; Alternative splicing.
 FT SIGNAL 1 22
 FT CHAIN 23 400
 FT DOMAIN 23 320
 FT TRANSMEM 321 346
 FT DOMAIN 347 400
 FT DISULFID 126 136
 FT DISULFID 165 178
 FT CARBOHYD 46 46
 FT CARBOHYD 54 54
 FT CARBOHYD 99 99
 FT CARBOHYD 123 123
 FT CARBOHYD 135 135
 FT CARBOHYD 182 182
 FT CARBOHYD 195 195
 FT CARBOHYD 223 223

FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 216 233 ERNPPSNVYRNCNTHHC -> GSLTSGCSRFHNSKTN
 FT VARSPLIC 234 400 MISSING (IN ISOFORM 6).
 FT VARSPLIC 271 286 INVSGLENYRNPSS -> VVLTSTGSLCTFMCSS (IN
 FT VARSPLIC 287 400 ISOFORM 4).
 FT VARSPLIC 316 400 MISSING (IN ISOFORM 4).
 FT VARSPLIC 318 333 GSDGNIGSVYIVLVLTGTLVGLTGLFRLRQLQFL
 FT VARSPLIC 334 400 PPVQIDKRLNDHEVEDETIMEEFTPEEGKGRREVLTVK
 FT VARSPLIC 376 400 EIT -> DHTLGIGTHPRGRRLPRGLDREGNLYRRCGRN
 FT SEQUENCE 400 AA; 46206 MW; D9025B981E41311D CRC64; GMDISASATGNCFLDDAVNLVLIIFYVLI (IN ISOFORM 5).
 FT DGNIGSVYIVLVLT -> LGTSGCSRFHNSKTN (IN ISOFORM 3).
 FT MISSING (IN ISOFORM 3).
 FT IWEFTPEEGKGRREVLTVK -> MGRQHRRCGN
 FT LYPFGPSGSGSPRLGSSSL (IN ISOFORM 2).
 FT SEQUENCE 400 AA; 46206 MW; D9025B981E41311D CRC64;
 Query Match 11.4%; Score 146.5; DB 1; Length 400;
 Best local Similarity 21.1%; Pred. No. 2.7e-05;
 Matches 52; Conservative 44; Mismatches 90; Indels 61; Gaps 10;
 QY 5 ILTPN-GNEDTADFLTPMTDLSVTLPLPVQCFVFNVMNCTMSSSPQPTNL 63
 DB 109 LLYPNSGEGTAQNF-----SCFIYNADIMCTW-ARPPAPRV 148
 QY 64 TLHWYKNSDNDKVOKSHYLFSEITSGCOLQ-----KKEIHLVQFEV 107
 DB 149 QYFLYINSKRRRIEIRCPYIQDSCGHVCHLDLSGLTSRNFVNGTIREIGI -QFF 206
 QY 108 VOLDDPRE-----PRRATQMLKQNLVTPAPENITLHLS--ESQLETMMNRLNHC 160
 DB 207 DSLDFTKKIEFRNPSPSVTVACNTTHCLVHW-KOPRTYQKLSYDFQYQDVRHKRTQPG 265
 QY 161 LEHLYOVRTDMDHWTQSDVYRHKFSLPSVDGKRTFVRSFNFLCSAGHWSWSH 220
 DB 266 TENLL-----INVSGLENRYNPSPSEPPAKSHVIRADVRIL---NWSWSSE 311
 QY 221 PIHWGNS 227
 DB 312 AIEFGSD 318
 RESULT 11
 PRLR_MELGA STANDARD; PRT; 831 AA.
 AC 091094; 091091; 091092;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Prolactin receptor precursor (PRL-R) (TPRLR).
 GN PRLR.
 OS Melagris gallinago (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
 OX NCBI_TaxID=9103;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Kidney;
 RX MEDLINE=97057891; PubMed=8902221;
 RA Zhou J.F., Zadorany D., Guemene D., Kuhnlein U.;
 RT "Molecular cloning, tissue distribution, and expression of the
 RT prolactin receptor during various reproductive states in Meleagris
 RT gallinago.";
 RL Biol. Reprod. 55:1081-1090(1996).
 RP SEQUENCE OF 82-121 AND 473-522 FROM N.A.
 RC TISSUE=Ovary;
 RA Pils G.R., You S.K., Foster D.N., el Halawani M.E.;

```

RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L76587; AAB01544.1; -
DR EMBL: U22947; AAB75038.1; -
DR EMBL: U22924; AAB75039.1; -
DR HSSP: P16471; IBP3.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR Pfam: PF00041; fn3; 4.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 438
FT TRANSMEM 439 459
FT DOMAIN 460 831
FT DOMAIN 25 122
FT DOMAIN 123 225
FT DOMAIN 228 325
FT DOMAIN 326 428
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315
FT CARBOHYD 335 335
SQ SEQUENCE 831 AA; 94394 MM; 220916320F77FA01 CRC64;

Query Match 11.3%; Score 145.5; DB 1; Length 831;
Best Local Similarity 24.3%; Pred. No. 8e-05;
Matches 53; Conservative 36; Mismatches 94; Indels 35; Gaps 10;

```

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AC Q90374;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Columba livia (Domestic Pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=9932;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CropSac;
RA MEDLINE=94283267; PubMed=7516866;
RX Chen X., Horseman N.D.;
RT "Cloning, expression, and mutational analysis of the pigeon prolactin
RL receptor.";
RL Endocrinology 135:269-276(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U07694; AAA20646.1; -
DR HSSP: P16471; IBP3.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam; PF00041; fn3; 4.
DR SMART; SM00060; FN3; 4.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 830
FT DOMAIN 24 439
FT TRANSMEM 440 460
FT DOMAIN 461 830
FT DOMAIN 25 122
FT DOMAIN 123 226
FT DOMAIN 229 326
FT DOMAIN 327 429
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 263 263
FT CARBOHYD 304 304
FT CARBOHYD 316 316
FT CARBOHYD 336 336
SQ SEQUENCE 830 AA; 94507 MM; 38074E83CDE69E9F CRC64;

Query Match 10.3%; Score 132.5; DB 1; Length 830;
Best Local Similarity 22.2%; Pred. No. 0.001;
Matches 44; Conservative 37; Mismatches 96; Indels 21; Gaps 7;

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Db 90 KNTNTWMTYNTINIVMAMNELGSSNDPOYVDTISYOPAPVNLSEFTSASTYTLAK 149
Qy 152 WNNRFL-----NHCEHLVQRTMDHSMTEOSVDYRHKFSLPSYDGKRTFRVRSRE 205
Db 150 WSPPLADVTNSHVYRLELRKPEKEEMETVSVGVQYKVNRLQAGKVVQVRCVL 209
Qy 206 NPLGSAQHSEWSHPH 223
Db 210 D-----IGEMSEWSSERH 222

RESULT 13
IL4R MOUSE STANDARD: PRT: 810 AA.
AC P16382;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
SE Interleukin-4 receptor alpha chain precursor (IL-4R-alpha).
IL4R OR IL4RA
Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 26-39; 162-179 AND 194-210.
RX MEDLINE=90030408; PubMed=2805066;
RA Moseley B., Beckmann M.P., March C.J., Idzerda R.L., Gimpel S.D.,
RA Vandenbos T., Friend D., Alpert A., Anderson D., Jackson J.,
RA Mignall J.M., Smith C., Gallis B., Slins J.E., Urdal D., Widmer M.B.,
RA Cosman D., Park L.S.;
RT "The murine interleukin-4 receptor: molecular cloning and
RT characterization of secreted and membrane bound forms.";
RL Cell 59:335-348(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90138976; PubMed=2405398;
RA Harada N., Castile B.E., Gorman D.M., Itoh N., Schreurs J.,
RA Barrett R.L., Howard M., Miyajima A.;
RT "Expression cloning of a cDNA encoding the murine interleukin 4
RT receptor based on ligand binding.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:857-861(1990).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR INTERLEUKIN-4. THE SOLUBLE FORM
CC OF THE IL-4 RECEPTOR MAY REPRESENT A REGULATORY MOLECULE SPECIFIC
CC FOR IL-4-DEPENDENT IMMUNE RESPONSES.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA CHAIN AND A COMMON GAMMA CHAIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: THERE ARE THREE CLASSES OF IL-4 RECEPTOR:
CC ONE CONTAINING EXTRACELLULAR, TRANSMEMBRANE, AND CYTOPLASMIC
CC DOMAINS, A SECOND LACKING THE CYTOPLASMIC DOMAIN, AND A THIRD
CC BEING A SECRETED FORM OF THE RECEPTOR. ALL THREE BIND IL-4.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M27959; AAA39299.1; -
CC EMBL: M27960; AAA39300.1; -
CC EMBL: M29854; AAA39297.1; -
CC PIR: A33380; A33380.
CC MGD: MGI:105367; IL4ra.
CC InterPro: IPR002966; CRLA.
CC InterPro: IPR003961; FN_III.
CC InterPro: IPR003531; Hematopo_receptor_S_FL.
CC Pfam: PF00041; fn3.1.
CC PROSITE: PS01355; HEMATOPO_REC_S_FL.1.
CC Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
KW

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FT SIGNAL 1 25
FT CHAIN 26 810 INTERLEUKIN-4 RECEPTOR ALPHA CHAIN.
FT DOMAIN 26 233 EXTRACELLULAR (POTENTIAL).
FT TRANSMDM 234 257 POTENTIAL.
FT DOMAIN 258 810 CYTOPLASMIC (POTENTIAL).
FT DISULFD 34 44 BY SIMILARITY.
FT DISULFD 75 87 BY SIMILARITY.
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC 225 230 HFDLP -> PSNENL (IN SECRETED ISOFORM).
FT VARSPPLIC 231 810 MISSING (IN SECRETED ISOFORM).
FT VARSPPLIC 258 810 MISSING (IN THIRD ISOFORM).
SQ SEQUENCE 810 AA; 87627 MW; 53699E01E938F6D CRC64;

Query Match 10.2%; Score 132; DB 1; Length 810;
Best Local Similarity 26.2%; Pred. No. 0.0011;
Matches 60; Conservative 28; Mismatches 107; Indels 34; Gaps 8;

Qy 14 TTADFLLTMTPLDISVSTPLDPEVQCFVNEVEMNCTW--NSSEPPITNLTHYWKNS 72
Db 10 TSVGCLILLVTGSGSIVLGEPT--TCSRDIYRTSGEWFLDSAVDCSSQLCHY----- 62
Qy 73 DNDKQKCSHYLFSEET-----SGCOLKKEIHLQYTFVQLODPREPRROATQML 124
Db 63 -----RLMFEFESNLLCIRNSASTVCCHMEMNRRVQSDRQMLMEHRQLMQSGSF 116
Qy 125 KLQNLVIFWAPENLTLKLSLSQELNWNPNFLNHCGL--EHLVQY----RTMDHSMTEQ 178
Db 117 SPSSGKPLADPNLTLTHNVSDEWLLTNWNLPSNNLTKKLILMVNISREDNPAEPIVY 176
Qy 179 SVDY---RHKSLSPVDQKRTFRVRSRPNLPGSAQHSEWSHPH 224
Db 177 NVTKEPRLSPIINTLMGCVYITARVRSQILTGT---MSWSPSITW 222

RESULT 14
CYRB MOUSE STANDARD: PRT: 896 AA.
AC P26955;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cytokine receptor common beta chain precursor.
GN CSF2RB OR CSF2RB1 OR AIC2B OR IL3RBL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90319131; PubMed=1695379;
RA Gorman D.M., Itoh N., Yamamura T., Schreurs J., Yonehara S.,
RA Yahara I., Arai K., Miyajima A.;
RT "Cloning and expression of a gene encoding an interleukin 3 receptor-
RT like protein: identification of another member of the cytokine
RT receptor gene family.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5459-5463(1990).
CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5
CC AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC

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[illegible]

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CC      PROLACTIN.
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC      -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce).
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: L02549; AAA51417.1; -.
DR      HSSP: P14787; 1AN3.
DR      InterPro: IPR002996; CRIA.
DR      InterPro: IPR003961; FN_III.
DR      InterPro: IPR003528; Hematopo_receptor_L_F1.
DR      Pfam: PFE0041; fn3; 2.
DR      SMART: SM00060; FN3; 2.
DR      PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
KW      Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT      SIGNAL 1 24 POTENTIAL.
FT      CHAIN 25 581 PROLACTIN RECEPTOR.
FT      DOMAIN 25 234 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 235 258 POTENTIAL.
FT      DOMAIN 259 581 CYTOPLASMIC (POTENTIAL).
FT      DOMAIN 25 122 FIBRONECTIN TYPE-III 1.
FT      DOMAIN 123 227 FIBRONECTIN TYPE-III 2.
FT      DISULFID 36 46 BY SIMILARITY.
FT      DISULFID 75 86 BY SIMILARITY.
FT      CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE 581 AA; 65153 MW; 7385C0DD656BE139 CRC64;

Query Match 9.4%; Score 121.5; DB 1; Length 581;
Best Local Similarity 25.4%; Pred. No. 0.0055;
Matches 60; Conservative 30; Mismatches 69; Indels 77; Gaps 17;

OY      28 LSVSTL---PLRE---VOCFVFNVEYKNCWPNSSSE-PPQTNLTLLHYWKNSDNCKYOK 79
DB      17 LSVSTLNGOSPPEKKPLRYLKCPSRGKETTCWMEPEADGGLFTNTLYL-HKEGET-LIHE 74
OY      80 CSHLFESEETSG---COLQKKEHLILOYTFVOL-----QDPR-----EPRR 118
DB      75 CPDK-----TGSFNSCYFSKKHTSIKMYIYITAINIOMKGISSDPDLVYHYIYEPER 129
OY      119 QATOMLKION-----LVIWPAENLTLKLKLSQSLNNKNNFNLHCLEHLVOYR--- 168
DB      130 PANLTLELKHPEDRKKRYLTIKMSPPPTMT-----DYKSGV-----FTIYQEIRL 172
OY      169 -----TDMDSWTEQSVVDYRHKFSLSVSDGCKRTFRVRSFNFPLGSAQHSMS 219
DB      173 KPEKATDMEHFLKOTOLK-IFNL--YRQK-----YLVQIRCKPDHG--YMSMS 219

```

Search completed: June 28, 2002, 07:43:19
Job time: 154 sec

CC¹ -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 RL¹ MOL. CELL. ENDOCRINOI. 89:47-58(1992).

Fri Jun 28 07:58:58 2002

us-09-825-561a-4.rsp

Page 13

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:40:45 ; Search time 65.65 Seconds
(without alignments)
339.569 Million cell updates/sec

Title: US-09-825-561A-4

Perfect score: 1288
Sequence: 1 LNTIILPNNGEDTTADFL.....QHMSWSPHMGSNSTSKEN 232

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_71:*
2: pir1:*
3: pir2:*
4: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1288	100.0	369	2	A42565
2	1097	85.2	373	2	A55718
3	853.5	66.3	369	2	I49280
4	168.5	13.1	426	2	JC7773
5	159	12.3	897	1	A39255
6	150	11.6	831	2	U01655
7	146.5	11.4	400	2	S06945
8	145.5	11.3	333	2	S13684
9	136.5	10.6	896	2	I56563
10	135.5	10.5	378	2	S50040
11	132.5	10.3	830	2	I50455
12	132	10.2	810	1	A33380
13	125	9.7	896	1	A35782
14	121.5	9.4	581	2	I45971
15	119.5	9.3	800	1	S13575
16	118	9.2	415	2	S12357
17	116	9.0	878	1	A40091
18	114	8.9	440	2	JL0144
19	114	8.9	460	2	JL0145
20	113	8.8	420	2	S21052
21	112	8.7	918	2	A36337
22	110.5	8.6	359	2	JC7280
23	110.5	8.6	551	2	A30342
24	109.5	8.5	292	2	I77525
25	109.5	8.5	303	2	I77524
26	109.5	8.5	608	2	I53269
27	108.5	8.4	310	2	A29884
28	108.5	8.4	412	2	A41070
29	108.5	8.4	610	2	A34631

30	108.5	8.4	610	2	A36116	prolactin receptor
31	107	8.3	335	2	A40267	interleukin-5 rece
32	105	8.2	539	2	A35052	interleukin-2 rece
33	104.5	8.1	286	2	S50039	granulocyte-macrop
34	104.5	8.1	917	2	I49699	glycoprotein 130 -
35	98.5	7.6	918	2	A44257	interleukin-6 sign
36	97.5	7.6	608	2	S33823	sonatotropin recep
37	97.5	7.6	825	1	A60386	interleukin-4 rece
38	96.5	7.5	625	2	S35317	hematopoietic grow
39	96.5	7.5	626	2	S37622	proto-oncogene - m
40	95.5	7.4	288	2	B59405	prolactin receptor
41	95.5	7.4	376	2	A59405	prolactin receptor
42	95.5	7.4	622	2	A40144	prolactin receptor
43	95.5	7.4	630	2	I51086	prolactin receptor
44	94.5	7.3	26926	2	I38344	titin, cardiac mus
45	94	7.3	537	2	B46535	interleukin 2 rece

ALIGNMENTS

```

RESULT
1
A42565
interleukin-2 receptor gamma chain - human
C:Species: Homo sapiens (man)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: A42565; A46591; I54332
R:Trakeshita, T.; Asao, H.; Ohtani, K.; Ishii, N.; Kumaki, S.; Tanaka, N.; Munakata, H
Science 257, 379-382, 1992
A:Title: Cloning of the gamma chain of the human IL-2 receptor.
A:Reference number: A42565; M0ID:92335883
A:Accession: A42565
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-369 <TAK>
A:Cross-references: GB:I12183; NID:9307056; PIDN:AAA59145.1; PID:9219890
A:Experimental source: MOLT beta lymphoid cells
A:Note: sequence extracted from NCBI backbone (NCBIP:109167)
R:Noguchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J.
J. Biol. Chem. 268, 13601-13608, 1993
A:Title: Characterization of the human interleukin-2 receptor gamma chain gene.
A:Reference number: A46591; M0ID:93293887
A:Accession: A46591
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: GB:I12183; NID:9307056; PIDN:AAA59145.1; PID:9307058
R:Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.;
Hum. Mol. Genet. 2, 1099-1104, 1993
A:Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-11
A:Reference number: I54332; M0ID:94004847
A:Accession: I54332
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RE2>
A:Cross-references: GB:I19546; NID:9349631; PIDN:AC37524.1; PID:9349632
C:Genetics:
A:Gene: GDB:IL2RG; SCIDXL1; IMD4
A:Cross-references: GDB:134807; OMIM:308380
A:Map position: Xq13.1-Xq13.1
A:Insertions: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3
A:Note: defects are associated with an X-linked form of severe combined immunodeficie
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; immunodeficiency; severe combined immunod
Query Match 100.0%; Score 1288; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 8.8e+100;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LNTIILPNNGEDTTADFLITMPDLSYSTLPDEVOCFVFNVEYMCCTNNSSEPO 60
DB 23 LNTIILPNNGEDTTADFLITMPDLSYSTLPDEVOCFVFNVEYMCCTNNSSEPO 82

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Oy      61  TNLTLHHYKNSDNDKVKQCSHYLFSEETITSCGLOKKEIHLVOTFPVQLODDPREPRQA 120
          |||
Db      83  TNLTLHHYKNSDNDKVKQCSHYLFSEETITSCGLOKKEIHLVOTFPVQLODDPREPRQA 142

Oy      121 TOMLKLQNLVLPWAPENLTLLKLSQSQLELNMNRFNLHNCLEHLVQYRTDMDSWTEQSV 180
          |||
Db      143 TOMLKLQNLVLPWAPENLTLLKLSQSQLELNMNRFNLHNCLEHLVQYRTDMDSWTEQSV 202

Oy      161 DYRKHFSLPSVDGOKRYTFYRVRSRNPPLCGSAQNMHSEMSHPILHMGSTNTSKEN 232
          |||
Db      203 DYRKHFSLPSVDGOKRYTFYRVRSRNPPLCGSAQNMHSEMSHPILHMGSTNTSKEN 254

RESULT  2
A55718
Interleukin-2 receptor gamma chain precursor - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 23-Jul-1999
Accession: A55718
Henthorn, P.S.; Somberg, R.L.; Pimiani, V.M.; Puck, J.M.; Patterson, D.F.; Felsburg, F.
Genomics 23, 69-74, 1994
A:Title: IL-2Rgamma gene microdeletion demonstrates that canine X-linked severe combined
A:Reference numbers: A55718; MUID:95130114
A:Accession: A55718
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-373 <HEX>
A:Cross-references: GB:UD04361; NID:9517411; PIDN:AAC48403.1; PID:9517412
C:Superfamily: Interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication

Query Match      85.2%; Score 1097; DB 2; Length 373;
Best Local Similarity 82.8%; Pred. No. 7.1e-84;
Matches 192; Conservative 24; Mismatches 16; Indels 0; Gaps 0;

Oy      1  INTTLTPENGNDTADPEFLTTPMPSLSVSTLPREVOCEVFVFNENYNCNTWNSSEBOP 60
          |||
Db      23  LNSTYPMFNGNNDTRPDEFLLATPSETLSVSLPLPEVQCFVFNENYNCNTWNSSEBOP 82

Oy      61  TNLTLHHYKNSDNDKVKQCSHYLFSEETITSCGLOKKEIHLVOTFPVQLODDPREPRQA 120
          |||
Db      83  TNLTLHHYKNSDNDKVKQCSHYLFSEETITSCGLOKKEIHLVOTFPVQLODDPREPRQA 142

Oy      121 TOMLKLQNLVLPWAPENLTLLKLSQSQLELNMNRFNLHNCLEHLVQYRTDMDSWTEQSV 180
          |||
Db      143 TOMLKLQNLVLPWAPENLTLLKLSQSQLELNMNRFNLHNCLEHLVQYRTDMDSWTEQSV 202

Oy      161 DYRKHFSLPSVDGOKRYTFYRVRSRNPPLCGSAQNMHSEMSHPILHMGSTNTSKEN 232
          |||
Db      203 DYRKHFSLPSVDGOKRYTFYRVRSRNPPLCGSAQNMHSEMSHPILHMGSTNTSKEN 254

RESULT  3
A49280
Interleukin-2 receptor gamma chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
Accession: A49280; A47514; JN0775; S37582; I53398
R:Caao, X.; Kozak, C.A.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993
A:Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) gene
A:Reference numbers: A47514; MUID:93391374
A:Accession: A49280
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <CAO>
A:Cross-references: EMBL:U021795; NID:9727349; PIDN:AAA64279.1; PID:9727350
A:Accession: A47514
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-369 <RE2>

```

A:Cross-references: GB:J20048; NID:g404067; PIDN:AAA3286.1; PID:g404068
R:Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.
Biochem. Biophys. Res. Commun. 193, 356-363, 1993
A:Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of fu
A:Reference number: JN0592; MUID:93277575
A:Accession: JN0592
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-369 <K0M>
A:Cross-references: DDBJ:DJ1565; NID:g303684; PIDN:BA02760.1; PID:g303685
R:Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
Gene 130, 303-304, 1993
A:Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
A:Reference number: JN0775; MUID:93366191
A:Accession: JN0775
A:Molecule type: mRNA
A:Residues: 1-369 <K0B>
A:Cross-references: GB:DJ13821; NID:g436045; PIDN:BA02974.1; PID:g436046
R:Chiu, R.K.; Dougherty, G.J.
submitted to the EMBL Data Library, October 1993
A:Description: Regulation of CD4-mediated cellular adhesion by the IL-2 R gamma chain
A:Reference number: S37582
A:Accession: S37582
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-350, 'S', 352-366, 'S', 368-369 <CHI>
A:Cross-references: EMBL:X75337
R:Disanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de
Bur, J. Immunol. 24, 3014-3018, 1994
A:Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosoma
A:Reference number: 153398; MUID:95104285
A:Accession: 153398
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-369 <R8S>
A:Cross-references: GB:S75852; NID:g861554; PIDN:AB32904.1; PID:g661555
C:Genetics:
A:Gene: IL-2rgamma
A:Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
A:Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHMS2), bet
eptors.
C:Function:
A:Description: receptor for interleukin-2
A:Pathway: Interleukin-2 stimulated growth and differentiation of T cells, B cells, N
C:Superfamily: Interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein
F:1-32/Domain: signal sequence #status predicted <SIG>
F:23-369/Product: interleukin-2 receptor gamma chain #status predicted <MAT>
F:256-284/Domain: transmembrane #status predicted <TM>
F:71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status predict

RESULT 4
JC7773
IL-13Ralpha 1 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: JC7773
R:Pierlot, C.; Beniquel, L.; Begue, A.; Khalife, J.
Biochem. Biophys. Res. Commun. 287, 969-976, 2001
A:Title: Expression of a functional IL-13Ralpha by rat B cells.
A:Reference number: JC7773; PMID:11573960
A:Accession: JC7773
A:Molecule type: mRNA
A:Residues: 1-426 <PIE>
A:Cross-references: GB:AY044251
C:Comment: This protein is an functionally binding protein involved in B cell proliferation
C:Genetics:
A:Gene: IL-13ralphal

	Query Match	13.1%	Score 168.5;	DB 2;	Length 426;
	Best Local Similarity	25.5%;	Prod. 1,7e-06;		
	Matches 54;	Conservative 30;	Mismatches 101;	Indels 27;	Gaps
Qy	37	EVQCFVENEVYMNCTWNSSEPPQ-TNLTTHYWKNSDNDKVKQCSHYLFSEETSCQL	95		
Db	129	ELOCQWHLNLSYMKSCWMLPGKMTSDPTNTLYLYY--SSLGSLQCCN--IHREGHICSF	183		
Qy	96	OKKEI---HLYQTFVYLODDRPREPRAQTOYMLKQNIYIPAPENLTLHKISEQELNM	152		
		:::	:::	:::	:::
		:::	:::	:::	:::
Db	186	KLTKESTNEEHHNIIQIMKADNAGKIRISYKIVSTSNVKGEPPIKHLF-LKNCALTYQM	244		
Qy	153	NN--RFLNHCLEHLVQYRTDDHDSMTESQVDRHK-----FSLPSVDGQ	194		
Db	245	KNPQFSSRCLSEYEYVSTQDTSYNSNLSLEVEDKCONSEFEDRMGASCQFISPGVLYN	304		
Qy	195	KRYTFRVRSRNPIC-GSAQIMSEKSHIIMG	225		
Db	305	TYVTIVRVAKTKKLCFDNDLMSNSELSTIG	336		

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RESULT      5
A39255
Cytokine receptor common beta chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 02-Sep-1997
C:Accession: A39255
R:Hayashida, K.; Kitamura, T.; Gorman, D.M.; Arai, K.; Yokota, T.; Miyajima, A.
Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990
T:Title: Molecular cloning of a second subunit of the receptor for human granulocyte-macrophage colony-stimulating factor
I:Reference number: A39255; MUID:91086571
A:Accession: A39255
A:Molecule type: mRNA
A:Residues: 1-897 <HAY>
A:Cross-references: GB:M38275
C:Comment: The human high-affinity IL-3, IL-5, and GM-CSF receptors have ligand-specific
C:Genetics:
A:Gene: GDB:CSF2RB
A:Cross-references: GDB:126838; OMIM:138981
A:Map position: 22q13.1-22q13.1
C:Superfamily: Interleukin-3 receptor beta chain; cytokine receptor homology
C:Keywords: alternative splicing; cytokine receptor; duplication; transmembrane protein
F:17-897/Product: cytokine receptor common beta chain #status predicted <SIG>
F:17-443/Domain: extracellular #status predicted <EXT>
F:35-232/Domain: cytokine receptor homology <CRS1>
F:250-431/Domain: cytokine receptor homology <CRS2>
F:444-460/Domain: transmembrane #status predicted <TM>
F:461-897/Domain: intracellular #status predicted <INT>

```

Query Match	12.3%;	Score 159;	DB 1;	Length 897;
Best Local Similarity	26.4%;	Pred. NO. 2.6e-05;		
Matches	55;	Conservative	40;	Mismatches 79;
			Indels	34;
			Gaps	12;

[illegible]

```

RESULT      6
J01655
prolactin receptor precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-Jul-2000
C:Accession: J01655
R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA
A:Reference number: J01655; MUID:93075121
A:Accession: J01655
A:Molecule type: mRNA
A:Residues: 1-831 <TAN>
A:Cross-References: DDBJ:J013154; NID:9222848; PIDD:BA002439.1; PID:9222849
A:Experimental source: Kidney
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-831/Product: prolactin receptor #status predicted <MAT>
F:36-219/Domain: cytokine receptor homology <CRS1>
F:239-425/Domain: cytokine receptor homology <CRS2>
F:439-466/Domain: transmembrane #status predicted <TM>
F:559, 91,100,112,133,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (cov

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Query Match	11.6%	Score 150	DB 2	length 831
Best Local Similarity	25.0%	Pred. No. 0.00013		
Matches	50	Conservative	34	Mismatches 90; Indels 26; Gaps 9;
Qy	38	VOCFVFNVYMCCTWNSSSE-PQPTNLTLLHYWYKMSNDKQVCKSHYLFSEETSG---	C	93
Db	34	ICRSLDEKETFCGWMKPGSDGGLPTNYTL-FYKSDSEETIECPDYR----	TSGPNSC	86
Qy	94	QIQCKRIHIXQFVVOQLDQPREPRQAT--QMLKIQNIYIPAPENLTLLH-KLSSQEL		150
Db	87	YENKNTSPWTFENLTIVATNIGSNSSDPQVDVYTSIQPSVNLNLETKRSANIMYL		146
Qy	151	--NMNNRPL-----NHCLHLYQVRYTDMDSHTEQSDVDYRHKFSLPVSDGGRYTFEYRS		203
Db	147	WAKWSPLLADASSNLYLHYELRIKPEEKKEWETISVGQTCQINRLNAGRYVQVYRC		206
Qy	204	RFPNPLCGSAQHSWSESHPIH		223
Db	207	TLDP-----GEWSEWSEERH		221

RESULT 7
S06945
nucleocyte-macrophage colony-stimulating factor receptor A precursor - human
Alternative names: GM-CSF receptor alpha chain; hemopoietic growth factor receptor
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
C:Accession: S06945; A11286; A44474
R:earing, D.P.; King, J.A.; Gough, N.M.; Nicola, N.A.
EMBO J. 8, 3667-3676, 1989

[illegible]

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A:Residues: 1333 <ASh>
A:Cross-references: EMBL:X54935; NID:g31860; PIRN:CAA38697.1; PID:g31861
R.Raines, M.A., Liu, L., Qian, S.G., Joe, V.: DiPersio, J.F.; Golde, D.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 8203-8207, 1991
A>Title: Identification and molecular cloning of a soluble human granulocyte-macrophage
A:Reference number: A40989; MUID:91376112
A:Accession: A40989
A:Molecule type: mRNA
A:Residues: 314-333 <RAI>
A:Cross-references: GB:M73832

Query Match      11.3%; Score 145.5; DB 2; Length 333;
Best Local Similarity 21.1%; Pred. No. 0.0001;
Matches 52; Conservative 43; Mismatches 90; Indels 61; Gaps 10;

QY 5 ILTPN-GNEEDTADFLPTMTDLSVSTLPLEVOCFVFNVEYNCTMNSSSEPOPNL 63
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 109 ILYPNSGREGTAQNKF-----SCFIYNADMNCITW-ARGPRAPRDV 148
       :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 64 TLHYMKNSDNCKVKCASHYLFESEITSGCOLQ-----KKEIHLYQFV 107
       :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 149 QYFLIKRSKRRELRCPYIIDDSGTNYGHCHDNLGLSTRMYFLVNTSREIG--QFF 206
       :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 108 VOLQDPRE----PRQAOTMLKLQNLVIIPAWENLTILKLS--ESQLNNKNRFELNH 160
       :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 207 DSLILTPTKKIERENPPSNVTYRCNTTHCLVRW-KOPRTYOKLSYLDFOYLQVHNRKNTPG 265
       :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 161 LEHLIYQRDMHSMTEDSVDRHKFSLPYVGOKRYETFRYSRRNPICGSAGSHSEWSH 220
       :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 266 TENLL-----INVSGLDENRIPESSSPRAKHAKVITADRVILL---NWSSNSE 311
       :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 221 PIHWGS 226
       :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 312 AIEFGS 317

RESULT 9
15653 Interleukin-3 receptor beta-subunit - rat
C:Species: Rattus sp. (rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
C:Accession: 156563
J:Appel, K.; Butlini, M.; Sauter, A.; Gebicke-Haefer, P.J.
U.Neurosci 15, 5800-5809, 1995
A>Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia a
A:Reference number: 156563; MUID:95370942
A:Accession: 156563
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-896 <RES>
A:Cross-references: GB:S79263; MID:g1086954; PIRN:AAB35068.1; PID:g1086955
C:GeneInfo:
A:Gene: rIL-3RBeta
C:Superfamily: Interleukin-3 receptor beta chain; cytokine receptor homology
C:Keywords: cytokine receptor
F.39-235/Domain: cytokine receptor homology <CRS1>
F.253-433/Domain: cytokine receptor homology <CRS2>

Query Match      10.6%; Score 136.5; DB 2; Length 896;
Best Local Similarity 23.9%; Pred. No. 0.0019;
Matches 48; Conservative 41; Mismatches 83; Indels 29; Gaps 11;

QY 38 VOCFVNVEYNMCITMNSSSEPOPNLTLHYWKNSDNCKVKCASHYLFESEITSG----- 92
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 251 LOCFEPDGIOSLNCSEWEWMK-VTDVSFGLFESSSPKAGEKCSFYV--KELQASRYTRY 307
       :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 93 -COLQKKEIHLIQTFVVVOLQDPREPRAQTOMLKQNLVIIPAWENLTILKLSOLELN 151
   :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 308 HCSLNVSDPAHAISQTVTSVK-----RLDGKRTIESFN-HIQMNPTLMLTKNRRS-YSLH 360
       :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 152 WNNR-----FLNHCLLEHLVQYRTD--MDHSKTEDSVDRHKFSLPYVGOKRYETFRYS 203

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Db 361 WETOKKSYPIQIAHFQ--VOYKKKLDKRWEDSKTE--NLNHAHMDLPOLPEPTSYCARAVK 417
 Oy 204 RFPNLCGSAQHSEMSHPITH 224
 Db 418 KTIPEYKGL--WSEMSNNECTW 436

RESULT 10

S50040
 granulocyte-macrophage colony-stimulating factor receptor alpha-3 chain - human
 N:Alternate names: GM-CSF receptor alpha-3 chain; hematopoietic growth factor receptor
 C:Species: Homo sapiens (man)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
 C:Accession: S50040; S47568
 R:Hu, X.; Zuckerman, K.S.
 A:Title: Cloning and sequencing of the cDNAs encoding two alternative splicing-derived
 A:Description: Cloning and sequencing of the cDNA encoding alternative splicing variants
 A:Reference number: S50039
 A:Accession: S50040

Molecule type: mRNA

A:Residues: 1-378 <HUX>

A:Cross-references: EMBL:L29349; NID:q460284; PIDN:AAA60962.1; PID:q463107

R:Hu, X.; Emanuel, P.D.; Zuckerman, K.S.

Biochim. Biophys. Acta 1223, 306-308, 1994

A:Title: Cloning and sequencing of the cDNAs encoding two alternative splicing-derived

A:Reference number: S47567; MUID:94368898

A:Accession: S47568

A:Molecule type: mRNA

A:Residues: 241-315,317-378 <HUX>

A:Cross-references: EMBL:L29349

C:Genetics:

A:Gene: GM-CSF-RA3; CSF3RA

A:introns: 316/3

C:Keywords: alternative splicing; glycoprotein; growth factor receptor; transmembrane p

Query Match

Best Local Similarity 10.5%; Score 135.5; DB 2; Length 378;

Matches 50; Conservative 43; Mismatches 90; Indels 61; Gaps 10;

Oy 5 ILTPN-GNETPTADFLTPMTSLSVSLPLPEVOCFVFNENYNNCTNSSEPOPTNL 63

Db 109 LTIYNSRGSTAAQNF-----SCFLYNADLMCTV--AGCPAPAPRV 148

Oy 64 TLHWYKNSDNDKVOKCSHYLFSSEITSGCOLQ-----KKEIHLYQFV 107

Db 149 QYFLYINRSKRREIRCPYIYDSGTHVGHLDNLGLSRNFTLVNGTSREIGT--QPF 206

Oy 108 VOLODPRE-----PRCAOTOMLKLQMLVPMAPENLTILKLS--ESQLELNNNNRFLNHC 160

Db 207 DSLIDTRKIERFNPSPNVYRCNTTICLVLM--KQPTTYOKLSLIDPOYOLDVHRKNTOPG 265

Oy 161 LEHLVOYRTMDHSWTEQSVDRHKEFLSPVDGOKRYTFRVRSREPLCGSAQHSEMSH 220

Db 266 TENL-----INVSQDENRYNFPSSPRRAKHSKIRADVRIL-----NMSSWSE 311

Oy 221 PIHW 224

Db 312 AIEF 315

RESULT 11

I50455

prolactin receptor - pigeon

C:Species: Columba livia (domestic pigeon)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000

C:Accession: I50455

R:Chen, X.; Horseman, N.D.

Endocrinology 135, 269-276, 1994

A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.

A:Reference number: I50455; MUID:94283267

A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-830 <CHE>
 A:Cross-references: EMBL:U07694; NID:q466381; PIDN:AAA20646.1; PID:q466382
 C:Superfamily: cytokine receptor homology
 F:36-220/Domain: cytokine receptor homology <CRS1>
 F:240-426/Domain: cytokine receptor homology <CRS2>

Query Match

Best Local Similarity 10.3%; Score 132.5; DB 2; Length 830;

Matches 44; Conservative 37; Mismatches 96; Indels 21; Gaps 7;

Oy 38 VOCFVNEVYMNCTWNSSE-POPTNLTLHWYKNSDNDKVOKCSHYLFSSEITSGCOLQ 96

Db 34 IRCRSLEKETPSCWKKPGSDGGLPTVTL--FYSKDESEKIECPDYGMSG--PNSCYPD 89

Oy 97 KKEIHLYQFVVOLODPREPROAT--QMLKLQNLVPMAPENLTILH--KLSESOLELN 151

Db 90 KNHTNPMTITNITVYMANNEIGSNSDPOQYDVTSIYQPDAPVLSLETTSASTYLLAK 149

Oy 152 WNNRFL-----NHCEHLVOYRTMDHSWTEQSVDRHKEFLSPVDGOKRYTFRVRSR 205

Db 150 WSPPLADVTSNSHYRYELRLKPEKEKEWETVSGVQYQVYKVRNLAGVYVQVYCVL 209

Oy 206 NPLCGSAQHSEMSHPITH 223

Db 210 D-----IGEMSEMSERN 222

RESULT 12

A33380

interleukin-4 receptor precursor - mouse

N:Alternate names: IL-4 receptor

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 01-Dec-2000

C:Accession: A33380; B33380; C33380; A34861; I54232

R:Mosley, B.; Beckmann, M.P.; March, C.J.; Idzerda, R.L.; Gimpel, S.D.; Vandenbos, T.

Widmer, M.B.; Cosman, D.; Park, L.S.

Cell 59, 335-348, 1989

A:Title: The murine interleukin-4 receptor: molecular cloning and characterization of

A:Reference number: A90911; MUID:90030408

A:Accession: A33380

A:Molecule type: mRNA

A:Residues: 1-810 <MO1>

A:Cross-references: GB:M27959; NID:q198363; PIDN:AAA39299.1; PID:q309408

A:Accession: B33380

A:Molecule type: mRNA

A:Residues: 1-258 <MO2>

A:Accession: C33380

A:Molecule type: mRNA

A:Residues: 1-224; 'PSNENL' <MO3>

A:Cross-references: GB:M27960; NID:q198365; PIDN:AAA39300.1; PID:q309409

A:Note: three parts of this sequence, including the amino end of the mature protein, was con

acellular domain and may encode a soluble form of the receptor

R:Harada, N.; Castle, B.E.; Gorman, D.M.; Itoh, N.; Schreurs, J.; Barrett, R.L.; Howa

Proc. Natl. Acad. Sci. U.S.A. 87, 857-861, 1990

A:Title: Expression cloning of a cDNA encoding the murine interleukin 4 receptor base

A:Reference number: A34861; MUID:90138976

A:Accession: A34861

A:Molecule type: mRNA

A:Residues: 1-810 <HAR>

A:Cross-references: GB:M29854; NID:q198346; PIDN:AAA39297.1; PID:q309407

R:Wrighton, N.C.; Campbell, L.A.; Lee, F.D.

Growth Factors 6, 103-118, 1992

A:Title: The murine interleukin-4 receptor gene: Genomic structure, expression and po

A:Reference number: I54232; MUID:92265335

A:Accession: I54232

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-73; 'T', 75-333; 'P', 335-810 <RES>

A:Cross-references: GB:M64879; NID:q198359; PIDN:AA859727.1; PID:q198361

C:Genetics:
 A:Introns: 24/1; 71/2; 122/1; 172/3; 225/1; 258/2; 284/3; 301/2
 C:Superfamily: Interleukin-4 receptor; cytokine receptor; cytokine receptor; glycoprotein; transmembrane protein
 C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <S16>
 F:26-810/Product: Interleukin-4 receptor #status predicted <EXT>
 F:26-233/Domain: extracellular #status predicted <EXT>
 F:34-219/Domain: cytokine receptor homology <CRS>
 F:234-257/Domain: transmembrane #status predicted <TMM>
 F:258-810/Domain: intracellular #status predicted <INT>
 F:72,129,135,163,177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.2%; Score 132; DB 1; Length 810;
 Best Local Similarity 26.2%; Pred. No. 0.004;

Matches 60; Conservative 28; Mismatches 107; Indels 34; Gaps 8;

QY 14 TTADFELTPTDLSVSTLPPEVOCFVFNVEYKNCW-NSSSEPOPTNLTHWYKNS 72
 10 TSVGCLILLVTSGLSKVGEF--TCFSDYITSTCEMFLDSAYDCSSQLCLH----- 62
 73 DNDKVKQKSHYLFSEIT-----SGCQLOKKEIHLVQTFVVLQDPRRQATOML 124
 63 -----RLMFEFSEENITCIPRNSASTVCVCHMNNRPVQSDRYQWELWAHRQLMGCSF 116
 QY 125 KLONLVPAPEPNTLHKLSSEQLTMNNRFLNHL--EHLVQ----RTDMDSWTEQ 178
 117 SPQGNVPLAPNDLTLTNVSDMLTMNNLYPSNNLTKDLISMNIRSDNPAAFIY 176
 QY 179 SVDY---RHKFSLPYDQGRYTRVRSRPNPLCGSAQHMSESHPIH 224
 177 NVTKEPRLSFPINILMSGVYTVARVRSQILTG--WSEWSPSTW 222
 Db

RESULT 13

cytokine receptor common beta chain precursor - mouse
 A:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
 C:Accession: A35782

R:Gorman, D.M.; Itoh, N.; Kitamura, T.; Schreurs, J.; Yonehara, S.; Yahara, I.; Arai, K.
 Proc. Natl. Acad. Sci. U.S.A. 87, 5459-5463, 1990
 A:Title: Cloning and expression of a gene encoding an interleukin 3 receptor-like protei
 A:Reference number: A35782; MUID:90319131

A:Molecule type: mRNA
 A:Accession: A35782
 A:Residues: 1-896 <GOR>
 A:Cross-references: GB:M34397; NID:q191821; PIDN:AAA37204.1; PID:9309101

Comment: Mouse high-affinity IL-3, GM-CSF, and one class of high-affinity IL-3 recept
 Superfamily: Interleukin-3 receptor; cytokine receptor; cytokine receptor homology
 C:Keywords: cytokine receptor; duplication; transmembrane protein

F:1-22/Domain: signal sequence #status predicted <S16>
 F:23-896/Product: cytokine receptor common beta chain #status predicted <MAY>
 F:23-441/Domain: extracellular #status predicted <EXT>
 F:33-235/Domain: cytokine receptor homology <CRS1>
 F:233-434/Domain: cytokine receptor homology <CRS2>
 F:442-463/Domain: transmembrane #status predicted <TMM>
 F:464-896/Domain: intracellular #status predicted <INT>

Query Match 9.7%; Score 125; DB 1; Length 896;
 Best Local Similarity 23.1%; Pred. No. 0.017;

Matches 48; Conservative 36; Mismatches 82; Indels 42; Gaps 11;

QY 38 VOCGFVNEVYKNCWSSSEPOPTNLTHWYKNSDNDKVKQKSHYLFSEITSGQLQK 97
 251 LQCFDGIQSLHGWETW--TTGSVSFGLYRSPVPAPEKCSPV----- 296
 Db
 QY 98 KE---IHLVQTFVVLQDPRRQATOMLONLV-----IPAPENLTLHKLS 144
 297 KEPGASVYTRRHCSLPV-EPNHSQYTVSKHLEQKFIYSNHIQMEPRLNLTKNR 355
 QY 145 ESQLEMLMNNR-----FLNCHLEHLVQY---IDMDSWTEQSVDRHKSFLPSVDGQR 196

Db 356 DS-YSLHMEROKMAYSFIEHTFO--VOYKKKSDSWEDSKTE-NLDRAHMDLSOLEPDS 411
 QY 197 YTPVRSRFNPPLCGSAQHMSESHPIH 224
 412 YCARVKK--PISNYDGIKSKMSEETW 437
 Db

RESULT 14

prolactin receptor - bovine
 A:Species: Bos primigenius taurus (cattle)
 C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000
 C:Accession: I45971
 R:Scott, P.; Kessler, M.A.; Schuler, L.A.
 Mol. Cell. Endocrinol. 89, 47-58, 1992
 A:Title: Molecular cloning of the bovine prolactin receptor and distribution of prola
 A:Reference number: I45971; MUID:93246019

A:Accession: I45971
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-581 <SCO>
 A:Cross-references: GB:I02549; NID:q163617; PIDN:AAA51417.1; PID:q163618
 C:Genetics:
 A:Gene: PRLR
 C:Superfamily: cytokine receptor homology
 F:36-221/Domain: cytokine receptor homology <CRS>

Query Match 9.4%; Score 121.5; DB 2; Length 581;
 Best Local Similarity 25.4%; Pred. No. 0.02;
 Matches 60; Conservative 30; Mismatches 69; Indels 77; Gaps 17;

QY 28 LSVSTL---PLPE-----VOCGFVNEVYKNCWSSSE-POPTNLTHWYKNSDNDKVK 79
 17 LSVSLNGQSPPEKPKVYKCRSPGKETFTQWMEPGADGLPNTVLTLY-HKGEI-LIHE 74
 QY 80 CSHYLFSEITSG---CQLOKKEIHLVQTFVVLQDPRRQATOML 124
 75 CPDYK-----TGGNNSCYFSKRTSITKMWYIVVAINQMGISSDPLVHYVTVPEPP 129
 Db

QY 119 QATOMLKLON-----LVIPAPENLTLHKLSSEQLTMNNRFLNHL--EHLVQ----RTDMDSWTEQ 178
 130 PANLTLELKHEDKRPYLMKNSPPMT-----DYKSGW-----FIQYEIRL 172
 Db

QY 169 -----TMDHSWTRQSVYDRHKSFLPSVDGQGRYTRVRSRPNPLCGSAQHMSEMS 219
 173 KPERATWETHTFKQYOLK-IFNL--YPOQK--YLVOIRCKPDHG---YMSWS 219
 Db

RESULT 15
 S31575
 Interleukin-4 receptor - rat
 A:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: S31575
 R:Richier, G.; Hein, G.; Blankenstein, T.; Diamantstein, T.
 submitted to the EMBL data library, December 1992
 A:Reference number: S31575
 A:Accession: S31575
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-800 <RIC>
 A:Cross-references: EMBL:X69903; NID:q56390; PIDN:CAA49528.1; PID:q56391
 C:Superfamily: Interleukin-4 receptor; cytokine receptor homology
 C:Keywords: cytokine receptor

F:34-218/Domain: cytokine receptor homology <CRS>
 Query Match 9.3%; Score 119.5; DB 1; Length 800;
 Best Local Similarity 26.6%; Pred. No. 0.044;
 Matches 58; Conservative 19; Mismatches 88; Indels 53; Gaps 9;

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:40:45 ; Search time 43.94 Seconds

(without alignments)
128.965 Million cell updates/sec

Title: US-09-825-561a-4

Perfect score: 1288

Sequence: 1 LMTTILTPNGNEDTADPFL.....QHMSEMSPIHMGNTSKEN 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

tal number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1288	100.0	347	1	US-08-052-205-7 Sequence 7, Appli
2	1288	100.0	347	1	US-08-595-974-7 Sequence 7, Appli
3	1288	100.0	369	1	US-08-052-205-4 Sequence 4, Appli
4	1288	100.0	369	1	US-08-595-974-4 Sequence 4, Appli
5	1277	99.1	230	1	US-08-052-205-11 Sequence 11, Appli
6	1277	99.1	230	1	US-08-595-974-11 Sequence 11, Appli
7	1277	99.1	252	1	US-08-052-205-9 Sequence 9, Appli
8	1277	99.1	252	1	US-08-595-974-9 Sequence 9, Appli
9	853.5	66.3	369	2	US-08-424-224-2 Sequence 2, Appli
10	853.5	66.3	369	5	PCT-US94-02891-69 Sequence 69, Appli
11	207	16.1	380	1	US-08-609-572-4 Sequence 4, Appli
12	207	16.1	380	4	US-08-841-751-4 Sequence 4, Appli
13	207	16.1	380	4	US-08-846-340-4 Sequence 4, Appli
14	207	16.1	380	4	US-08-846-344-4 Sequence 4, Appli
15	198.5	15.5	383	4	US-08-609-572-2 Sequence 2, Appli
16	198.5	15.5	383	4	US-08-841-751-2 Sequence 2, Appli
17	199.5	15.5	383	4	US-08-846-340-2 Sequence 2, Appli
18	199.5	15.5	383	4	US-08-846-344-2 Sequence 2, Appli
19	178	13.8	427	4	US-08-969-125-9 Sequence 9, Appli
20	159	12.3	897	1	US-07-960-389-2 Sequence 2, Appli
21	150.5	11.7	552	1	US-08-243-010-6 Sequence 6, Appli
22	146.5	11.4	400	1	US-08-351-149-6 Sequence 6, Appli
23	146.5	11.4	400	1	US-08-384-828-6 Sequence 6, Appli
24	146.5	11.4	400	1	US-08-895-474-6 Sequence 6, Appli
25	126	9.8	606	4	US-09-523-217-97 Sequence 97, Appli
26	120	9.3	538	3	US-09-040-005-2 Sequence 2, Appli
27	120	9.3	538	4	US-09-522-217-115 Sequence 115, App

28	118	9.2	335	1	US-07-947-130-3 Sequence 3, Appli
29	118	9.2	335	1	US-08-421-822-3 Sequence 3, Appli
30	118	9.2	335	1	US-08-421-823-3 Sequence 3, Appli
31	118	9.2	398	1	US-07-757-390-6 Sequence 6, Appli
32	118	9.2	398	1	US-08-442-282-6 Sequence 6, Appli
33	118	9.2	398	1	US-08-442-281-6 Sequence 6, Appli
34	118	9.2	398	2	US-08-939-727-5 Sequence 5, Appli
35	118	9.2	415	1	US-07-757-390-5 Sequence 5, Appli
36	118	9.2	415	1	US-08-442-283-5 Sequence 5, Appli
37	118	9.2	415	1	US-08-442-281-5 Sequence 5, Appli
38	118	9.2	415	2	US-08-939-727-5 Sequence 5, Appli
39	115	8.9	315	1	US-07-757-390-8 Sequence 8, Appli
40	115	8.9	315	1	US-08-442-282-8 Sequence 8, Appli
41	115	8.9	315	1	US-08-442-281-8 Sequence 8, Appli
42	115	8.9	315	2	US-08-939-727-8 Sequence 8, Appli
43	115	8.9	332	1	US-07-757-390-7 Sequence 7, Appli
44	115	8.9	332	1	US-08-442-282-7 Sequence 7, Appli
45	115	8.9	332	1	US-08-442-281-7 Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-052-205-7
; Sequence 7, Application US/08052205
; Patent No. 5510259
; GENERAL INFORMATION:
; APPLICANT: SUGAMURA, KAZUO
; APPLICANT: TAKESHTA, TOSHIKAZU
; APPLICANT: ASAO, HIRONOBU
; APPLICANT: NAKAMURA, MASATAKA
; APPLICANT: SHIMAMURA, TOSHIRO
; APPLICANT: SUZUKI, MANABU
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OHION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/052,205
; FILING DATE: 19930422
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 104947/1992
; FILING DATE: 23-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ohion, No. 5510259man F.
; REGISTRATION NUMBER: 24, 618
; REFERENCE/DOCKET NUMBER: 10-615-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ. ID NO.: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-052-205-7

Query Match 100.0%; Score 1288; DB 1; Length 347;
 Best Local Similarity 100.0%; Pred. No. 9,5e-119;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTLILPNGNEDTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTMNSSSEPOP 60
 DB 1 LNTLILPNGNEDTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTMNSSSEPOP 60

QY 61 TNLTLHWYKNSDNDKQKCSHYLFSEITSGCOLQKKEHLVOTFYVOLDDPREPRROA 120
 DB 61 TNLTLHWYKNSDNDKQKCSHYLFSEITSGCOLQKKEHLVOTFYVOLDDPREPRROA 120

QY 121 TOMLKLONLVIWPAPENLTLHKLSSEQLMNMNRFNLHCLEHLVOTRTDMDHSWTEOSV 180
 DB 121 TOMLKLONLVIWPAPENLTLHKLSSEQLMNMNRFNLHCLEHLVOTRTDMDHSWTEOSV 180

QY 181 DYRHKFSLPVSDGQKRYTFVRSRFNPICGSAQHWSESHPIHMGNTSKEN 232
 DB 181 DYRHKFSLPVSDGQKRYTFVRSRFNPICGSAQHWSESHPIHMGNTSKEN 232

RESULT 2
 US-08-595-974-7
 ; Sequence 7, Application US/08595974
 ; Patent No. 5705608
 ; GENERAL INFORMATION:
 ; APPLICANT: SUGAMURA, KAZUO
 ; APPLICANT: TAKESHITA, TOSHIKAZU
 ; APPLICANT: ASAO, HIRONOBU
 ; APPLICANT: NAKAMURA, MASATAKA
 ; APPLICANT: SHIMAMURA, TOSHIRO
 ; APPLICANT: SUZUKI, MANABU
 ; APPLICANT: HAMURO, JUNJI
 ; TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ; ADDRESSEE: P.C.
 ; STREET: 1755 S. Jefferson Davis Highway, Suite 400
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/595,974
 ; FILING DATE: 06-FEB-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/052,205
 ; FILING DATE: 22-APR-1993
 ; APPLICATION NUMBER: JP 104947/1992
 ; FILING DATE: 23-APR-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Oblon, No. 5705608man F.
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 10-615-0X
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 413-3000
 ; TELEFAX: (703) 413-2220
 ; TELEX: 248855 OPAT UR
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 347 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-595-974-7

Query Match 100.0%; Score 1288; DB 1; Length 347;
 Best Local Similarity 100.0%; Pred. No. 9,5e-119;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTLILPNGNEDTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTMNSSSEPOP 60
 DB 1 LNTLILPNGNEDTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTMNSSSEPOP 60

QY 61 TNLTLHWYKNSDNDKQKCSHYLFSEITSGCOLQKKEHLVOTFYVOLDDPREPRROA 120
 DB 61 TNLTLHWYKNSDNDKQKCSHYLFSEITSGCOLQKKEHLVOTFYVOLDDPREPRROA 120

QY 121 TOMLKLONLVIWPAPENLTLHKLSSEQLMNMNRFNLHCLEHLVOTRTDMDHSWTEOSV 180
 DB 121 TOMLKLONLVIWPAPENLTLHKLSSEQLMNMNRFNLHCLEHLVOTRTDMDHSWTEOSV 180

QY 181 DYRHKFSLPVSDGQKRYTFVRSRFNPICGSAQHWSESHPIHMGNTSKEN 232
 DB 181 DYRHKFSLPVSDGQKRYTFVRSRFNPICGSAQHWSESHPIHMGNTSKEN 232

RESULT 3
 US-08-052-205-4
 ; Sequence 4, Application US/08052205
 ; Patent No. 5510259
 ; GENERAL INFORMATION:
 ; APPLICANT: SUGAMURA, KAZUO
 ; APPLICANT: TAKESHITA, TOSHIKAZU
 ; APPLICANT: ASAO, HIRONOBU
 ; APPLICANT: NAKAMURA, MASATAKA
 ; APPLICANT: SHIMAMURA, TOSHIRO
 ; APPLICANT: SUZUKI, MANABU
 ; APPLICANT: HAMURO, JUNJI
 ; TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ; ADDRESSEE: P.C.
 ; STREET: 1755 S. Jefferson Davis Highway, Suite 400
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/052,205
 ; FILING DATE: 19930422
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 104947/1992
 ; FILING DATE: 23-APR-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Oblon, No. 5510259man F.
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 10-615-0X
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 413-3000
 ; TELEFAX: (703) 413-2220
 ; TELEX: 248855 OPAT UR
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 369 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-052-205-4

Query Match	100.0%	Score 1288	DB 1	Length 369
Best Local Similarity	100.0%	Pred. No. 1e-1187		
Matches 232	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	LNTLTLPNGNEDTTADFFLTPTMTDSLSVSTLPLREYQCEFVENYEMNCNTSSSEDP	60	
Db	23	LNTLTLPNGNEDTTADFFLTPTMTDSLSVSTLPLREYQCEFVENYEMNCNTSSSEDP	82	
QY	61	TNLTTHWYKNSDNDKQKCHYLFESEITSGCOLKKEINHLYQFVYVLODRPRRQA	120	
Db	83	TNLTTHWYKNSDNDKQKCHYLFESEITSGCOLKKEINHLYQFVYVLODRPRRQA	142	
QY	121	TQMLKLOMLVTPMARENLTTLKLSQLELMWNNRFLNHCLEHLVQYRTDMDHSTEQSY	180	
Db	143	TQMLKLOMLVTPMARENLTTLKLSQLELMWNNRFLNHCLEHLVQYRTDMDHSTEQSY	202	
QY	181	DYRHKFSLPVSDGQKRYTFRVRSRRNPCLSGSQHHSSEMSHPRIHMSNSTKEN	232	
Db	203	DYRHKFSLPVSDGQKRYTFRVRSRRNPCLSGSQHHSSEMSHPRIHMSNSTKEN	254	

```

1 RESULT 4
2 US-08-595-974-4
3 : Sequence 4, Application US/0855974
4 : Patent No. 5705608
5 :
6 : GENERAL INFORMATION:
7 : APPLICANT: SUGAMURA, KAZUO
8 : APPLICANT: TAKESHITA, TOSHIAKAZU
9 : APPLICANT: ASAO, HIRONOBU
10 : APPLICANT: NAKAMURA, MASATKA
11 : APPLICANT: SHIMAMURA, TOSHIO
12 : APPLICANT: SUZUKI, MANABU
13 : APPLICANT: HAMURO, JUNJI
14 : TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
15 : NUMBER OF SEQUENCES: 21
16 :
17 : CORRESPONDENCE ADDRESS:
18 : ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
19 : ADDRESSEE: P.C.
20 : STREET: 1755 S.
21 : CITY: Arlington
22 : STATE: Virginia
23 : COUNTRY: U.S.A.
24 :
25 : ZIP: 22202
26 :
27 : COMPUTER READABLE FORM:
28 : MEDIUM TYPE: Floppy disk
29 : OPERATING SYSTEM: IBM PC compatible
30 : SOFTWARE: PatentIn Release #1.0, Version #1.25
31 :
32 : CURRENT APPLICATION DATA:
33 : APPLICATION NUMBER: US/08/595,974
34 : FILING DATE: 06-FEB-1996
35 :
36 : CLASSIFICATION: 435
37 :
38 : PRIOR APPLICATION DATA:
39 : APPLICATION NUMBER: US 08/052,205
40 : FILING DATE: 22-APR-1993
41 : APPLICATION NUMBER: JP 104947/1992
42 : FILING DATE: 23-APR-1992
43 :
44 : ATTORNEY/AGENT INFORMATION:
45 : NAME: Oblon, No. 5705608man F.
46 : REGISTRATION NUMBER: 24,618
47 : REFERENCE/DOCKET NUMBER: 10-615-0X
48 : TELECOMMUNICATION INFORMATION:
49 : TELEPHONE: (703) 413-3000
50 : TELEFAX: (703) 413-2220
51 :
52 : INFORMATION FOR SEQ ID NO: 4:
53 : SEQUENCE CHARACTERISTICS:
54 : LENGTH: 369 amino acids
55 : TYPE: amino acid
56 : TOPOLOGY: linear
57 :
58 : MOLECULE TYPE: protein
59 :
60 : US-08-595-974-4

```

	Query Match	100.0%;	Score 1288;	DB 1;	Length 369;
	Best Local Similarity	100.0%;	Pred. No. 1e-118;		
	Matches 233;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	LNTTILTPNGNEDTADFFLTITMPDLSVSLPLPEVOCFVFNVEYINCTWNSSSEPOP	60		
Db	23	LNTTILTPNGNEDTADFFLTITMPDLSVSLPLPEVOCFVFNVEYINCTWNSSSEPOP	82		
QY	61	TNLTLHWYKNSNDVOKCSHYLFESEITSCSOLÖKEIHLXYOTFVVOLODPEPERÖA	120		
Db	83	TNLTLHWYKNSNDVOKCSHYLFESEITSCSOLÖKEIHLXYOTFVVOLODPEPERÖA	142		
QY	121	TÖMLKLÖNLVI PVAPENLTLHKLSSESÖELMANNNEFLHMCHEHLVOYRTMDHSWTESQV	180		
Db	143	TÖMLKLÖNLVI PVAPENLTLHKLSSESÖELMANNNEFLHMCHEHLVOYRTMDHSWTESQV	202		
QY	181	DYRKFEFLPEVDDGOKRYTFPRVRSRRPFLPGSGQÖHMSSESHIIMGSMSTKEN	232		
Db	203	DYRKFEFLPEVDDGOKRYTFPRVRSRRPFLPGSGQÖHMSSESHIIMGSMSTKEN	254		

```

1      RESULT      5
2      US-08-052-205-11
3      ; Sequence 11, Application US/08052205
4      Patent No. 5510259
5      GENERAL INFORMATION:
6      APPLICANT: SUGAMURA, KAZUO
7      APPLICANT: TAKESHITA, TOSHIKAZU
8      APPLICANT: ASAO, HIRONOBU
9      APPLICANT: NAKAMURA, MASATKA
10     APPLICANT: SHIMAMURA, TOSHIRO
11     APPLICANT: SUZUKI, MANABU
12     APPLICANT: HAMURO, JUNJI
13     TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
14     NUMBER OF SEQUENCES: 21
15     CORRESPONDENCE ADDRESS:
16     ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
17     ADDRESSEE: P.C.
18     STREET: 1755 S. Jefferson Davis Highway, Suite 400
19     CITY: Arlington
20     STATE: Virginia
21     COUNTRY: U.S.A.
22     ZIP: 22202
23     COMPUTER READABLE FORM:
24     MEDIUM TYPE: Floppy disk
25     COMPUTER: IBM PC compatible
26     OPERATING SYSTEM: PC-DOS/MS-DOS
27     SOFTWARE: PatentIn Release #1.0, Version #1.25
28     CURRENT APPLICATION DATA:
29     APPLICATION NUMBER: US/08/052,205
30     FILING DATE: 19930422
31     CLASSIFICATION: 435
32     PRIOR APPLICATION DATA:
33     APPLICATION NUMBER: JP 104947/1992
34     FILING DATE: 23-APR-1992
35     ATTORNEY/AGENT INFORMATION:
36     NAME: Oblon, No. 5510259man F.
37     REGISTRATION NUMBER: 24,618
38     REFERENCE/DOCKET NUMBER: 10-615-0X
39     TELECOMMUNICATION INFORMATION:
40     TELEPHONE: (703) 413-3000
41     TELEFAX: (703) 413-2220
42     TELEX: 248855 OPAT UR
43     INFORMATION FOR SEQ ID NO: 11:
44     SEQUENCE CHARACTERISTICS:
45     LENGTH: 230 amino acids
46     TYPE: AMINO ACID
47     TOPOLOGY: linear
48     MOLECULE TYPE: protein
49     US-08-052-205-11

```

Query Match 99.1%; Score 1277; DB 1; Length 230;
Best Local Similarity 100.0%; Pred. No. 6,4e-118;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILPNGNEDTADFFLTMTPTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPP 60
DB 1 LNTTILPNGNEDTADFFLTMTPTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPP 60
QY 61 TNLTLHWYKNSDNDKVKCSHYLFSEETSGCQLOKKEHLHYQTFVVOLODPPRRQA 120
DB 61 TNLTLHWYKNSDNDKVKCSHYLFSEETSGCQLOKKEHLHYQTFVVOLODPPRRQA 120
QY 121 TOMLKQNLVTPWAPENLTILKLSQLELNMNRFNLNHCLEHLVQYRTDMDHSMTQSV 180
DB 121 TOMLKQNLVTPWAPENLTILKLSQLELNMNRFNLNHCLEHLVQYRTDMDHSMTQSV 180
QY 181 DYHKKFSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEMSHPIMHGSNTSK 230
DB 181 DYHKKFSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEMSHPIMHGSNTSK 230

RESULT 6
US-08-595-974-11
Sequence 11, Application US/08595974
Patent No. 5705608
GENERAL INFORMATION:
APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHITAKA
APPLICANT: ASAO, HIRONOBU
APPLICANT: NAKAMURA, MASATAKA
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: SUZUKI, MANABU
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,974
FILING DATE: 06-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,205
FILING DATE: 22-APR-1993
APPLICATION NUMBER: JP 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5705608man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-595-974-11

Query Match 99.1%; Score 1277; DB 1; Length 230;
Best Local Similarity 100.0%; Pred. No. 6,4e-118;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTILPNGNEDTADFFLTMTPTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPP 60
DB 1 LNTTILPNGNEDTADFFLTMTPTDLSVSTLPLPEVOCFVFNVEYMNCTWNSSEPP 60
QY 61 TNLTLHWYKNSDNDKVKCSHYLFSEETSGCQLOKKEHLHYQTFVVOLODPPRRQA 120
DB 61 TNLTLHWYKNSDNDKVKCSHYLFSEETSGCQLOKKEHLHYQTFVVOLODPPRRQA 120
QY 121 TOMLKQNLVTPWAPENLTILKLSQLELNMNRFNLNHCLEHLVQYRTDMDHSMTQSV 180
DB 121 TOMLKQNLVTPWAPENLTILKLSQLELNMNRFNLNHCLEHLVQYRTDMDHSMTQSV 180
QY 181 DYHKKFSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEMSHPIMHGSNTSK 230
DB 181 DYHKKFSLPSVDGQKRYTFRVRSRFPNPLCGSAQHSEMSHPIMHGSNTSK 230

RESULT 7
US-08-052-205-9
Sequence 9, Application US/08052205
Patent No. 5510259
GENERAL INFORMATION:
APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHITAKA
APPLICANT: ASAO, HIRONOBU
APPLICANT: NAKAMURA, MASATAKA
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: SUZUKI, MANABU
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/052,205
FILING DATE: 19930422
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5510259man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-052-205-9

Query Match 99.1%; Score 1277; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 7.3e-118;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTITLPGNDTADFLTMTPTDLSVSTLPLPEVOCFVFNVEVMNCTMNSSEPOP 60
DB 23 LNTTITLPGNDTADFLTMTPTDLSVSTLPLPEVOCFVFNVEVMNCTMNSSEPOP 82
QY 61 TNLTLHWKNSDNDKVKQCSHYLFSEBITSGCOLQKKEHLVOTFYVOLQDPRERRQA 120
DB 83 TNLTLHWKNSDNDKVKQCSHYLFSEBITSGCOLQKKEHLVOTFYVOLQDPRERRQA 142
QY 121 TOMLKLQNLVTPWAPENLTLHKLSEQLMLMNNRFLNHCHLEHLVQYRTDMDHSTEQSV 180
DB 143 TOMLKLQNLVTPWAPENLTLHKLSEQLMLMNNRFLNHCHLEHLVQYRTDMDHSTEQSV 202
QY 181 DYHKKESLSVDGQKRYTFRVRSRPNPLCGSAOHMSEKSHPIHWSNTSK 230
DB 203 DYHKKESLSVDGQKRYTFRVRSRPNPLCGSAOHMSEKSHPIHWSNTSK 252

RESULT 8

US-08-595-974-9
Sequence 9, Application US/08595974
Patent No. 5705608

GENERAL INFORMATION:

APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHIKAZU
APPLICANT: ASAO, HIRONOBU
APPLICANT: NAKAMURA, MASATAKA
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: SUZUKI, MANBU
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Highway, Suite 400
City: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,974
FILING DATE: 06-FEB-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/052,205
FILING DATE: 22-APR-1993
APPLICATION NUMBER: JP 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, No. 5705608mar F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEO ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-595-974-9

Query Match 99.1%; Score 1277; DB 1; Length 252;
Best Local Similarity 100.0%; Pred. No. 7.3e-118;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNTTITLPGNDTADFLTMTPTDLSVSTLPLPEVOCFVFNVEVMNCTMNSSEPOP 60
DB 23 LNTTITLPGNDTADFLTMTPTDLSVSTLPLPEVOCFVFNVEVMNCTMNSSEPOP 82
QY 61 TNLTLHWKNSDNDKVKQCSHYLFSEBITSGCOLQKKEHLVOTFYVOLQDPRERRQA 120
DB 83 TNLTLHWKNSDNDKVKQCSHYLFSEBITSGCOLQKKEHLVOTFYVOLQDPRERRQA 142
QY 121 TOMLKLQNLVTPWAPENLTLHKLSEQLMLMNNRFLNHCHLEHLVQYRTDMDHSTEQSV 180
DB 143 TOMLKLQNLVTPWAPENLTLHKLSEQLMLMNNRFLNHCHLEHLVQYRTDMDHSTEQSV 202
QY 181 DYHKKESLSVDGQKRYTFRVRSRPNPLCGSAOHMSEKSHPIHWSNTSK 230
DB 203 DYHKKESLSVDGQKRYTFRVRSRPNPLCGSAOHMSEKSHPIHWSNTSK 252

RESULT 9

US-08-424-224-2
Sequence 2, Application US/08424224
Patent No. 5912173

GENERAL INFORMATION:

APPLICANT: LEONARD, WARREN J.
TITLE OF INVENTION: MORINE IL-2R CDNA AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,224
FILING DATE:

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/121,435
FILING DATE: 14-SEPT-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4061051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 369
TYPE: AMINO ACID
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: PROTEIN
HYPOTHEICAL: NO
ORIGINAL SOURCE:
ORGANISM: MORINE
INDIVIDUAL ISOLATE: IL-2R
US-08-424-224-2

Query Match 66.3%; Score 853.5; DB 2; Length 369;
 Best Local Similarity 67.2%; Pred. No. 5.2e-76;
 Matches 156; Conservative 33; Mismatches 42; Indels 1; Gaps 1;

Oy 2 NTTLTPNGNEDTADFLITMPTDLSVSTLPPEVOCFVFNENYKNCWSSSEPOPT 61
 Db 24 SSKVMSANEDIKADILITSTAPHLAPILPEVOCFVFNENYKNCWSSSEPOAT 83
 Oy 62 NLTLYWYKNSDNDKVKCSHYLFSEETISGCOLKEIHLHYQTFVVOLODPPRRQAT 121
 Db 84 NLTLYWYKNSDNDKVKCSHYLFSEETISGCOLKEIHLHYQTFVVOLODPPRRQAV 143
 Oy 122 QMLKQLVTPAPENLTLAKLSESOLELNNRFL-NHCEHLVOYRTDMSWTEQSV 180
 Db 144 QKMLQNLVTPAPENLTLNSLSEOLELRKMSRIKRCQLQYLVOYRSNRDSMTLLIV 203
 Oy 181 DYRKESLPVSDGOKRYTFRVRSRNPICGSAQMSKSWQPEVHWSHTVEEN 232
 Db 204 NHEPFSLPVDELKRTFRVRSRNPICGSAQMSKSWQPEVHWSHTVEEN 255

SULT 10
 PCT-US94-02891-69

Sequence 69, Application PC/TUS9402891

GENERAL INFORMATION:

APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS

APPLICANT: REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN

APPLICANT: SERVICES

APPLICANT: OFFICE OF TECHNOLOGY TRANSFER, NATIONAL

APPLICANT: INSTITUTES OF HEALTH, BOX 077, BETHESDA, MARYLAND 20892 USA

TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVE.

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORD PERFECT # 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/02891

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/031,143

FILING DATE: 12-MAR-1993

APPLICATION NUMBER: 08/121,435

FILING DATE: 14-SEPT-1993

ATTORNEY/AGENT INFORMATION:

NAME: WILLIAM S. FEILER

REGISTRATION NUMBER: 26,728

REFERENCE/DOCKET NUMBER: 206-4061

TELEPHONE: 212-758-4800

TELEFAX: 212-751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 369

TYPE: AMINO ACID

TOPOLOGY: UNKNOWN

MOLECULE TYPE: PROTEIN

DESCRIPTION: NO

ORIGINAL SOURCE:

ORGANISM: MURINE

INDIVIDUAL ISOLATE: IL-2R

PCT-US94-02891-69

Query Match 66.3%; Score 853.5; DB 5; Length 369;
 Best Local Similarity 67.2%; Pred. No. 5.2e-76;
 Matches 156; Conservative 33; Mismatches 42; Indels 1; Gaps 1;

Oy 2 NTTLTPNGNEDTADFLITMPTDLSVSTLPPEVOCFVFNENYKNCWSSSEPOPT 61
 Db 24 SSKVMSANEDIKADILITSTAPHLAPILPEVOCFVFNENYKNCWSSSEPOAT 83
 Oy 62 NLTLYWYKNSDNDKVKCSHYLFSEETISGCOLKEIHLHYQTFVVOLODPPRRQAT 121
 Db 84 NLTLYWYKNSDNDKVKCSHYLFSEETISGCOLKEIHLHYQTFVVOLODPPRRQAV 143
 Oy 122 QMLKQLVTPAPENLTLAKLSESOLELNNRFL-NHCEHLVOYRTDMSWTEQSV 180
 Db 144 QKMLQNLVTPAPENLTLNSLSEOLELRKMSRIKRCQLQYLVOYRSNRDSMTLLIV 203
 Oy 181 DYRKESLPVSDGOKRYTFRVRSRNPICGSAQMSKSWQPEVHWSHTVEEN 232
 Db 204 NHEPFSLPVDELKRTFRVRSRNPICGSAQMSKSWQPEVHWSHTVEEN 255

RESULT 11

US-08-609-572-4

Sequence 4, Application US/08609572

Patent No. 5710023

GENERAL INFORMATION:

APPLICANT: Collins, Mary

APPLICANT: Donaldson, Debra

APPLICANT: Filz, Lori

APPLICANT: Neben, Tamlyn

APPLICANT: Whitters, Mathew

APPLICANT: Wood, Clive

TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: MA

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/609,572

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: BROWN, Scott A.

REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: G15268

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 380 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-609-572-4

Query Match 16.1%; Score 207; DB 1; Length 380;
 Best Local Similarity 25.4%; Pred. No. 1.9e-12;
 Matches 60; Conservative 46; Mismatches 106; Indels 24; Gaps 9;

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Oy 9 NGNETTADFEJTLNTPMDTSLSVSTLPLPEVOCAFENENYANCNMSSSEDP-----T 61
    | | | : | : |
Db 115 NGSE VOSSMAETTYWISPOCIPETKYQDMOCYVYNNQYHLLCSW-----KPGIYLLDT 167
    | | | : | : |
Oy 62 NLTLLHYWAKNSDNDRVOKCSHYLPSEETITSGCOLKKEHLHYGFVYVOLLDPRE--PRQ 119
    | | | : | : | : | : |
Db 168 NYNLFWEYEGDLH--ALQGVQYIKADQNGICRRPYLEADYKDFYICVANGSSENKPIRS 225
    | | | : | : | : | : |
Oy 120 ATOMKILQNLVTPAPENLTLHKLSQSOLBNMN---NRFNLHCLEHLVOYRTDDHSHWT 176
    | : | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 226 SYTFEOLQNLINPKPRLPYLFTFRSSCEIKLWISLPGPIPARCFDEIAREID--DTLLV 284
    | : | | | : | : | : | : | : | : | : | : | : | : | : | : |
Oy 177 EQSDVYRRKESLPEVDQGRKTFEVRGRPNPLGSAQAHEWSHPHIM--CSNYSKE 231
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 285 TAYVE-NETTYLTKTNETTROLCEFYVRSKVINYSCDDGCIWSEWSKQOCWESEDL3K 339
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

```

1      RESULT      12
2      US-08-841-751-4
3      Sequence 4, Application US/08841751
4      Patent No. 6214559
5      GENERAL INFORMATION:
6      APPLICANT: Collins, Mary
7      APPLICANT: Donaldson, Debora
8      APPLICANT: Fitz, Lori
9      APPLICANT: Neben, Tamlyn
10     APPLICANT: Whilters, Matthew
11     APPLICANT: Wood, Clive
12     TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
13     NUMBER OF SEQUENCES: 9
14     CORRESPONDENCE ADDRESS:
15     ADDRESSEE: Genetics Institute, Inc.
16     STREET: 87 Cambridgepark Drive
17     CITY: Cambridge
18     STATE: MA
19     COUNTRY: USA
20     ZIP: 02140
21     COMPUTER READABLE FORM:
22     MEDIUM TYPE: Floppy disk
23     COMPUTER: IBM PC compatible
24     OPERATING SYSTEM: PC-DOS/MS-DOS
25     SOFTWARE: PatentIn Release #1.0, Version #1.25
26     CURRENT APPLICATION DATA:
27     APPLICATION NUMBER: US/08/841,751
28     FILING DATE:
29     CLASSIFICATION:
30     PRIOR APPLICATION DATA:
31     APPLICATION NUMBER: 08/609,572
32     FILING DATE:
33     ATTORNEY/AGENT INFORMATION:
34     NAME: Brown, Scott A.
35     REGISTRATION NUMBER: 32,724
36     REFERENCE/DOCKET NUMBER: G15268
37     TELECOMMUNICATION INFORMATION:
38     TELEPHONE: (617) 498-8224
39     TELEFAX: (617) 876-5851
40     INFORMATION FOR SEQ. ID NO: 4:
41     SEQUENCE CHARACTERISTICS:
42     LENGTH: 380 amino acids
43     TYPE: amino acid
44     TOPOLOGY: linear
45     MOLECULE TYPE: protein
46     US-08-841-751-4

```

	Query Match	16.1%	Score 207;	DB 4;	Length 380;	
	Best Local Similarity	25.4%;	Pred.	0.19e-12;		
	Matches	60;	Conservative	46;	Mismatches 106;	Indels 24; Gaps 9;
Qy	9	NGNEDTTADFLLTTPMTDLSYSVILPELVOCFVNVEYMNCTNNSSSEPQ-----T	61			
		:: :: :	:	:	:	:
Db	115	NGSE-VQSSMAETWISPGGIPETKRVDDMDCVYYNMWGLLCSW-----RKGIQVLDT	167			

```

Oy      62 NLTLLHWKNSNDNKVKQKCSHYLSEETSSCOLOKKEHILHYQFVVOLODPRE--PRQ 119
        ||| ||| : : : : : ||| : : : : :
Db      168 NMYLFEWEGDHH--ALCCVDYIADGONICRPPYLEASDYKDFYLCVNGSSENKPIRS 225
        ||| ||| : : : : : ||| : : : : :
Oy      120 ATQMKLONLVIAPAPENULTHKISEQOLETNWV--NRFNLHOLEHLYQYRTDWDHWSWT 176
        : : ||| : ||| : ||| : : : : : : : : : : : : : : : : : : : :
Db      226 STFFQLOINIVKPLPPYLYLTTRSSCCIKTKWSPILGPIPARCFEYELIRED--DTLLV 284
        : : ||| : ||| : ||| : : : : : : : : : : : : : : : : : : : :
Oy      177 EOSVDYRHRKFSPLSDVGOKRYTFRYSRFRNPLGCSAOWMSWSPHFW-GSNTSKE 231
        : : : : : : : : : ||| : ||| : : : : : : : : : : : : : :
Db      285 TAYVE-NETYLTKLTNETNRQQLCFVYRSKVNIIYICSDDGITMSWMSKQCGWEGEDLSKK 339
        : : : : : : : : : ||| : ||| : : : : : : : : : : : : : :

```

```

13
US-08-846-340-4
Sequence 4, Application US/08846340
Patent No. 6248714
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debora
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Wilters, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,340
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609,572
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-846-340-4

```

Query March 16, 1981	Score 207	DB 4	Length 380
Best Local Similarity	25.4%	Pred. No. 1,982	
Matches 60	Conservative 46	Mismatches 16	Indels 24
		Gaps 9	

QY	9	NGNEDTTADFLITMTPTDLSVSTLPLEPVCFVFNVNYMCTNNSSEFP-----T	61
Db	115	NGSE-VOSSAETTYWISPOGIPETKRVQMDCVYNNMVLCLSS-----KPGIYALDT	167
QY	62	NLTLYWYKNSDDKVKQCSHYLFSEETISGCOLKREIHLVYQTFVYVQLDDPRE--PRRO	119
Db	168	NYNLYEYECLELDH--ALQCVDIKADGNQICREFYELASDKPQFYICVNGSSENRPIIS	225

,Fri, Jun 28 07:58:57 2002

us-09-825-561a-4.ra1

Page 9

Job time: 54 sec

4

5

6

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:40:45 ; Search time 63.41 seconds
(without alignments)
632.942 Million cell updates/sec

Title: US-09-825-561a-4
Perfect score: 1288
Sequence: 1 LNTTILTPNGNEDTTADFFL.....QHWSESHPIHWSNTSKEN 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% Length	DB ID	Description
1	283.5	22.0	343	13 Q9DEQ1	Q9DEQ1 oncorhynchu
2	259.5	20.1	404	13 Q90X88	Q90X88 oncorhynchu
3	213	16.5	386	6 Q95UF0	Q951F0 canis famli
4	199.5	15.5	383	11 Q88786	Q88786 mus musculu
5	178	13.8	427	4 Q96BB4	Q96BB4 homo sapien
6	172.5	13.4	405	6 Q95LE1	Q951F1 canis famli
7	159.5	12.4	371	4 Q9HC73	Q9HC73 homo sapien
8	141.5	11.0	279	4 Q9UDY5	Q9UDY5 homo sapien
9	139	10.8	890	11 Q9Z1A0	Q9Z1A0 cavia porce
10	137.5	10.7	415	11 Q9Z0K4	Q9Z0K4 cavia porce
11	137.5	10.7	881	13 Q95J19	Q95J19 xenopus lae
12	137	10.6	349	6 Q97597	Q97597 bos taurus
13	136.5	10.6	896	11 Q64146	Q64146 rattus norv
14	136	10.6	232	4 Q9H5R3	Q9H5R3 homo sapien
15	130	10.1	611	13 Q91BF6	Q91BF6 xenopus lae
16	130	10.1	611	13 Q9PT10	Q9PT10 xenopus lae

17	130	10.1	810	11 Q54690	Q54690 mus musculu
18	128	9.9	810	11 Q60583	Q60583 mus musculu
19	125	9.7	611	13 Q9PT89	Q9PT89 xenopus lae
20	124.5	9.7	918	13 Q9W6U9	Q9W6U9 gallus gall
21	121.5	9.4	296	6 Q18880	Q18880 bos taurus
22	120.5	9.4	229	11 Q91W8	Q91W8 rattus norv
23	120.5	9.4	801	11 Q9TW8	Q9TW8 rattus norv
24	120	9.3	538	4 Q9HBE5	Q9HBE5 homo sapien
25	120	9.3	538	4 Q9HB91	Q9HB91 homo sapien
26	119.5	9.3	800	11 Q63257	Q63257 rattus norv
27	118.5	9.2	370	11 Q9J1C7	Q9J1C7 mus musculu
28	117.5	9.1	359	11 Q9JMD5	Q9JMD5 mus musculu
29	116.5	9.0	359	11 Q9J3H8	Q9J3H8 mus musculu
30	115.5	9.0	359	11 Q9J3H8	Q9J3H8 mus musculu
31	115	8.9	414	11 Q9J3H8	Q9J3H8 mus musculu
32	115	8.9	414	11 Q920B8	Q920B8 rattus norv
33	113.5	8.8	626	13 Q90W67	Q90W67 cynops pyr
34	113	8.8	420	4 Q14633	Q14633 homo sapien
35	112	8.7	396	4 Q14631	Q14631 homo sapien
36	112	8.7	602	13 Q90ZB0	Q90ZB0 carassius a
37	111	8.6	625	6 Q9XS92	Q9XS92 trichosurus
38	110	8.5	425	11 Q9JMD5	Q9JMD5 mus musculu
39	110	8.5	600	13 Q9PT89	Q9PT89 carassius a
40	109.5	8.5	608	11 Q9J3H8	Q9J3H8 mus musculu
41	107	8.3	333	4 Q15469	Q15469 homo sapien
42	106.5	8.3	422	4 Q75462	Q75462 homo sapien
43	106	8.2	227	6 Q9GLW3	Q9GLW3 ursus marit
44	105	8.2	581	6 Q46561	Q46561 ovis aries
45	105.5	8.2	422	4 Q90HNS	Q90HNS homo sapien

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	343 AA.
Q9DEQ1	Q9DEQ1:			
AC	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	CYTOKINE RECEPTOR COMMON GAMMA CHAIN.			
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;			
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.			
OX	NCBI_TaxID=8022;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-21287902; PubMed-11394690;			
RA	Mang T., Secombes C.J.;			
RT	"Cloning and expression of a putative common cytokine receptor gamma			
RT	chain gene in rainbow trout (Oncorhynchus mykiss)."			
RL	Fish and Shellfish Immunol. 11:233-244(2001).			
DR	EMBL; AJ276623; CAC09429.2; -			
KW	Receptor.			
SO	SEQUENCE 343 AA; 39486 MW; ED8429E7534B21EB CRC64;			

Query Match	22.0%; Score 283.5; DB 13; Length 343;
Best Local Similarity	30.9%; Pred. No. 3.7e-19;
Matches	59; Conservative 37; Mismatches 88; Indels 7; Gaps 4;
QY	36 PEVCGFVNEVYMCNTSSSEPOPTNLTFLHYWKKSDNDKYOKGSHYFSEITNSGOL 95
DB	23 PNVCLTINDYVNCISSEOSIPE-VNFT--FSSNFTDNDMECTTYTQESYAVGCR 79
QY	96 QKKRIHLYQFVVYVLODPREPRROATQMLQNLVTPAPENLTLEKLSQLEINMNR 155
DB	80 SYDSDFRFLTKLV--HNNMSYVODHNLKSMVXLPVNLVSMNKPDLNLTWNNS 136
QY	156 FLNCLHLYQYRDMQHSWTEOSVDYRHKFSLPVSDGQKRTFRFRSFPNLCGSAQHW 215
DB	156 FLNCLHLYQYRDMQHSWTEOSVDYRHKFSLPVSDGQKRTFRFRSFPNLCGSAQHW 215

D_b 137 KMFCESEVRRIKNSD-KMKTSPRNEQYAVAFPLKSSRETFQVRRARVNDMGSEEFN 155
O_y 216 SEMSHPIHNGS 226
 | | | | | | | |
D_b 196 SEMSQPIQWDS 206

RESULT	2
ID	090XP8
AC	090XP8;
DT	01-DEC-2001 (TREMblrel. 19, Created)
DT	01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT	01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE	INTERLEUKIN 13 RECEPTOR ALPHA-2.
OS	Oncorhynchus mykiss (Rainbow trout) (<i>Salmo gairdneri</i>).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostomi;
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX	[1]
RN	NBI_Taxid=6022;
RA	SEQUENCE FROM N.A.
RT	Lockeyer A.E., Jones C.S., Noble L.R., Verspoor E., Holland J.,
RT	Secombes C.J.;
RL	"Isolation and characterization of a putative interleukin 13 receptor
DR	alpha-2 sequence from rainbow trout (<i>Oncorhynchus mykiss</i>).",
KW	Submitted (MAR-2001) to the EMBL/GenBank/DBO databases.
EMBL:	AF361437; AAL26921.1; -.
REceptor.	
40A	AA: 46728 MW: 489B7E3FAFFB6D6 CRC64:
SEQUENCE	

Query Match	20.1%	Score 259.5	DB 13	Length 404
Best Local Similarity	27.9%	Pred. No. 9e-17		
Matches 56	Conservative 44	Mismatches 88	Indels 13	Gaps 6

QY	40	CEVFNVEYNMCTNNSS--SEPOPTNLILHWYKNSNDKVCOKSHYLTSELTSGCOLQK	98
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	143	CVFKQKFMCTMETGLEPTQSLSYWRH--EMEAECPOYIINSNGVROCKTTE	200
QY	99	EIHLYOTF--VQLODPREPRQATOMKLQWLYFAPAPENLTLHKISEQELANW--N	153
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	201	SLSEDFPNICINSSSEYVLLSAFFSLQIQWYAPALIEVHLHESAPDRLOQMDLPN	260
QY	154	NRLTNLCLEHLVQYRTD--WDHSWTQSVQVYHHRKFSPLPSVDGQKRYFYRSPRNP	211
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	261	ERIPRHCLEVEARREGVGGOPFLQRRNTNEMTLTSLMDGARRKCFVRASRHHYCAD	320
QY	212	AQHWSEMSHPIHMGSTSKEN	232
		: : : : : : : : : : : : : : : : : : : : : : : : :	
	321	RGFWSDMS--HWSCHSDTES	338

RESULT	3		
O95LF0			
AC	O95LF0	PRELIMINARY;	PRT; 386 AA.
DT	01-DEC-2001 (Tremblre, 19, Created)		
DT	01-DEC-2001 (Tremblre, 19, Last sequence update)		
DT	01-DEC-2001 (Tremblre, 19, Last annotation update)		
DE	INTERLEUKIN 13 RECEPTOR ALPHA CHAIN 2.		
GN	IL13RA2.		
OS	Canis familiaris (Dog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
CC	NCBI_Taxid=9615;		
NP	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=2128753; PubMed=1138954;		
RA	Tang L.;		
RT	"Molecular cloning of canine IL-13 receptor alpha chain (alpha and		
RT	alpha) cDNAs and detection of corresponding mRNAs in canine		
RT	tissues.";		

RL Vet Immunol, Immunopathol. 79:181-195(2001).
 DR EMBL: AF314533; AAL14887.1; -.
 KN Receptor.
 SQ SEQUENCE 386 AA; 45110 MW; A16FDF2DD023ED95 CRC64;

Query Match	16.5%;	Score 213;	DB 6;	Length 386;
Best Local Similarity	25.8%;	Pred. No. 2.4e-12;		
Matches	61;	Conservative	38;	Mismatches 107; Indels 30; Gaps 8;

```

OY 3 TTTILT--PNCNEDDTTAFFLTITPTDTSLSVTLPLLEVOACGVFVFNATNCSSNPPQ--P 60
      ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 125 TTYWTSPOGRRET-----KIDMDICYIIMYQIYVCSMKRGMGVAFED 160
      ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
OY 61 TNLTLHWYNSNDKRVKCRSHYLEFSEETSGCOLKKEIHLVOTEFVLODPRE--PRR 110
      ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 166 TNYOLFHWYIGDLHS--ACTDIYIKVNGKNMGCRFPLESSDYKDFYICVNSSSEQPR 220
      ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
OY 119 QATOMELKQNLVTPAPENILTLHKLESOLELNN--NRELNHCLEHLVQYRTDMDSHW 170
      ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 224 PSYRIFQLOQIVAMPDPDYLSLTIVKNSEIINILKNMMPKGRIPACAFYEIEFTED--GTW 280
      ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
OY 176 TEGSVDIRAHSLSIPVDGOKRTTFRVRSRFRNPLCGSAQHSNSHPIRMGNSNTSKE 231
      ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 283 VTTVEVEIDITTSNESOK--LCFIVRSKVNIVYCSDOIGNSWSEDECKMGIDTWE 337
      ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

```

RESULT	4		
ID	088786	PRELIMINARY;	PRT; 383 AA.
AC	088786;		
DT	01-NOV-1998 (TReMBLrel. 08, Created)		
DT	01-NOV-1998 (TReMBLrel. 08, Last sequence update)		
DE	01-DEC-2001 (TReMBLrel. 19, Last annotation update)		
GN	IL-13 RECEPTOR ALPHA 2 (INTERLEUKIN 13 RECEPTOR, ALPHA 2).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C3H/HEJ; TISSUE=THYMUS;		
RX	MEDLINE=98391042; Pubmed=9723226;		
RA	Donaldson D.D., Whittiers M.J., Fitz L., Neben T.Y., Finnerly H.,		
RA	Henderson S.L., O'Hara R.M. Jr., Beier D.R., Turner K.J., Wood C.R.,		
RA	Collins M.;		
RT	"The murine IL-13 receptor alpha 2: molecular cloning,		
RT	characterization, and comparison with murine IL-13 receptor alpha 1.",		
RL	J. Immunol. 161:2317-2324(1998).		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RP	Straussberg R.;		
RL	Submitted (Feb.-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; U65747; AAC33240.1; "		
DR	EMBL; BC003723; AAH03723.1; "		
DR	HSSP; P16471; 1BP3.		
DR	MGI; MGI:127954; IL13ra2.		
DR	InterPro; IPR002966; CRIA.		
DR	InterPro; IPR003532; Hematopo_receptor_S_F2.		
DR	ProSite; PS01356; HEMATOPO_RFC_SF; UNKNOWN_1.		
SW	RECEPTOR		
SW	SEQUENCE 383 AA; 44482 MW; C25212325C47E35B CRC64;		

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Query Match      15.5% Score 199.5; DB 11: Length 383;
Best Local Similarity 25.7%; Pred. No. 4,7e-11;
Matches 55; Conservative 40; Mismatches 108; Indels 11; Gaps
7;
```


QY 84 LFESEITSCQLOKKEIHLVQTFVVL--QDPRPRRQATOMLKLQNLVTPWAPENLTLH 141
 182 LQDEKNVCKSLNLDSSDYKDFECVNGSSKLEPRSSYFVQLQNLVTPWAPENLTLH 241
 QY 142 KISESLELNMN--NRFLNHCLEHLVQYRTDMDSHMTQESVDYHKKSLPSVDCQKRYT 198
 Db 242 VENSIDIRKMSPPGGFIPRCYTYEVIRED-DISW-ESATYDKMDKLKRRANSEDL 299
 QY 199 FVRSRFPNPLCGSAOHMSHPIHWSNTSKEN 232
 Db 300 FVFRKVNITVCAADGCIWSEMSSECEGEGYTPDS 333

RESULT 5
 Q96BB4 PRELIMINARY; PRT; 427 AA.
 AC Q96BB4:
 NT 01-DEC-2001 (TREMBLREL. 19, Created)
 01-DEC-2001 (TREMBLREL. 19, Last sequence update)
 DE INTERLEUKIN 13 RECEPTOR, ALPHA 1.
 OS Homo sapiens (Human).
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON ADENOCARCINOMA;
 RA Strausberg R.;
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC015768; AAL15768.1; -
 KW Receptor.
 SQ SEQUENCE 427 AA; 48676 MW; E6A42F7466A39A09 CRC64;

Query Match 13.8%; Score 178; DB 4; Length 427;
 Best Local Similarity 26.7%; Pred. No. 6.2e-09;
 Matches 58; Conservative 38; Mismatches 83; Indels 38; Gaps 11;

QY 37 EVOCCFNNVEYMCNTNNSSEPOP-TNLTLHWYKNSDNDKYOKSHYLFSEITSGC-- 93
 Db 131 ELDCIMHNLSYKMGCSMLPGRNTSPDTNLTLYWMSL-EKIHQCEN-IFREGYFGCSF 187
 QY 94 QLOKKEIHLVQTFVVL--QDPRPRRQATOMLKLQNLVTPWAP-ENLTLHKLSESOLE 149
 Db 188 DLKRVKSSPEQSHVOIWKNDGKIKPSFNIVPLTSVKKPDPHKNLSF--NDPLY 244
 150 LNMNN--RFLNHCLEHLVQYRTDMDSHMT-----EQSVYRHKFSLP 189
 Db 245 VQENPQNFISRL---FYEVVNSQETHNVFYVQAKCENDEFEFERNVENTSCFVVP 300
 QY 190 SYDQKRYTFRVRSRFPNPLCGSAOHMSHPIHWS 225
 Db 301 GVLDPDLNTVIRVKTNKLCEYEDDKLMSWQSMGIG 337

RESULT 6
 Q95LFL PRELIMINARY; PRT; 405 AA.
 AC Q95LFL:
 DT 01-DEC-2001 (TREMBLREL. 19, Created)
 DT 01-DEC-2001 (TREMBLREL. 19, Last sequence update)
 DE INTERLEUKIN 13 RECEPTOR ALPHA CHAIN 1 (FRAGMENT).
 GN IL13RA1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_Taxid=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21287533; PubMed=11389954;
 RA Tang L.;

RT "Molecular cloning of canine IL-13 receptor alpha chain (alpha1 and
 RT alpha2) cDNAs and detection of corresponding mRNAs in canine
 RT tissues.";
 RT Vet. Immunol. Immunopathol. 79:181-195(2001).
 DR EMBL; AF314532; AAL14886.1; -
 KW Receptor.
 FT NON_TER
 SQ SEQUENCE 405 AA; 46328 MW; 926ELAC7BE5E3F42 CRC64;

Query Match 13.4%; Score 172.5; DB 6; Length 405;
 Best Local Similarity 25.7%; Pred. No. 1.9e-08;
 Matches 68; Conservative 36; Mismatches 110; Indels 51; Gaps 13;

QY 1 LNTFTLPNGNEDDTADFTLTPTDLSVSTLP-----LPEYQCFVNEVMNCWTW 52
 Db 68 LNERICLQVQSCSTNE---SDNPSILVEKCPPEPGDPEAVTELOQWHLNLSYKCTW 124
 QY 53 NNSSEPOP-TNLTLHWYKNSDNDKYOKSHYLFSEITSGC-----QKKEIHLVQ 104
 Db 125 LPGRNTSPDTNLTLYW--SLGKILQCED-IYREGQIHGCFALTNLKDSSFEQHSVO 181
 QY 105 TFVVLQDPRPRRQATOMLKLQNLVTPWAPENLTLHKLSESOLELNMN--RFLNHCLE 162
 Db 182 ---IMVKDNARKIRPSFNIVPLTSVKKPDPHKKRLF-FQNGMLYQWKNPQNFYSRL- 236
 QY 163 HLVOYRTDMDSHMT-----QSVYRHK-----FSLPSVDCQKRYTFRVRSR 204
 Db 237 ---SYQEVNNSQETHNDFYVEAKQNSFEFGNIEGTICFWPGVLPDLNTVIRVR 293
 QY 205 FNPPLCGSAOHMSHPIHWSNT 228
 Db 294 TNKLCYEYDKLMSWQSMGIGENT 318

RESULT 7
 Q9HC73 PRELIMINARY; PRT; 371 AA.
 AC Q9HC73:
 DT 01-MAR-2001 (TREMBLREL. 16, Created)
 DT 01-MAR-2001 (TREMBLREL. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)
 DE CYTOKINE RECEPTOR CRL2 PRECURSOR (IL-XR) (THYMIC STROMAL LYMPHOPOIETIN
 DE PROTEIN RECEPTOR TSLP).
 GN CRL2 OR IL-XR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21134329; PubMed=11237741;
 RA Zhang W., Wang J., Wang Q., Chen G., Zhang J., Chen T., Wan T.,
 RA Zhang Y., Cao X.;
 RT "Identification of a novel type I cytokine receptor CRL2
 RT preferentially expressed by human dendritic cells and activated
 RT monocytes.";
 RT Biochem. Biophys. Res. Commun. 281:878-883(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311890; PubMed=11418668;
 RA Reche P.A., Soumelis V., Gorman D., Menon S., Zurawski S.,
 RA Johnston J., Liu Y.-J., Spits H., de Waal-Malefyt R., Bazan J.F.,
 RA Kastelein R.A.;
 RT "Human thymic stromal lymphopoietin preferentially stimulates myeloid
 RT cells.";
 RL J. Immunol. 167:336-343(2001).

DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR003532; Hematopo_receptor_S_F2.
 DR Pfam: PF00041; fn3; 1.
 DR PROSITE: PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
 DR Signal: Receptor.
 FT SIGNAL 1 17
 FT CHAIN 18 415
 FT SEQUENCE 415 AA; 46913 MW; 41BA4BA597B31CD4 CRC64;

Query Match 10.7%; Score 137.5; DB 11; Length 415;
 Best Local Similarity 23.3%; Pred. No. 4.5e-05;
 Matches 54; Conservative 41; Mismatches 102; Indels 35; Gaps 11;

QY 8 PNGEDTTADFFLTMTPTDLSVSTPLPEVQCFVNEVMCTNNSSSE-PQPTNLTLH 66
 DB 118 PGSPGTSIVLACTTNTAASNTYLNKSEVS-----LHCTWLACGADPEDTQFLY 169
 DB 67 YWYKNSNDKVKCKSHLSEELTS--GCQLQKKEIH--LYQTFVYQLODPREPRKQAT 121
 DB 170 YRY---GPTWEECOEY--SKDILSRNTACWPPRTFLHSKARDRLAVHVC--SSNHAT 220
 QY 122 -----QMLKLNLYIPWAPENLTLLKLSQLELMNN--NRLNCHLEHLVQRTDMDH 173
 DB 221 IKPFQQLFDQAIQDPNPMDVTA-ETEGSRSLQIQKQKPSARPIHCFEVEVACIKTKDY 279
 QY 174 SMTQSDYDKHKRSLPSVDQKRTFRVRSRFPPLCGSAQHSEMSHPIMWG 225
 DB 280 YQVEKTTT---NAFVSTTDGVSRTSIQVRAVSPHCRAMGLMSKMSQPYVVG 328

RESULT 11
 ID 057519 PRELIMINARY; PRT; 881 AA.
 AC 057519;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE GP130P1.
 GN XGP130.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
 OC Xenopodidae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 PP SEQUENCE FROM N.A.
 PR Chen J., Grace A., Chien K.R.;
 RT "Partial characterization of putative Xenopus gp130.",
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF041845; AAC03531.1; -.
 DR HSSP: P40189; 1B0U.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR Pfam: PF00041; fn3; 4.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR SEQUENCE 881 AA; 99003 MW; 7DE7942D211138A0 CRC64;

Query Match 10.7%; Score 137.5; DB 13; Length 881;
 Best Local Similarity 23.3%; Pred. No. 0.00011;
 Matches 51; Conservative 31; Mismatches 94; Indels 43; Gaps 10;
 QY 18 FFLTMTPTDLSVSTPLPEVQCFVNEVMCTNNSSSE-PQPTNLTL-HYWKNSDND 75
 DB 115 FFLGLPDPKPT-----NLCTIVYNODMLCTMDPGRPNTLPNTYTLISHMAHGAN- 166
 QY 76 KVKCKSHYLESEELTSCQLQKKEIHLYQTFVYQLODPREPRKQATQMLKLO--NLVYIW 133
 DB 167 -----YCRGANNSCITHSPGFYIDTTFQVEATNELGIQKSELTLLDPVNTIKPN 217

QY 134 APENTLTKLISE-----SOLELMNNRFLN-HCLEHLVQYR----TMDHSWTEQSY 180
 DB 218 PQQ-----LSELSSLELPAALKIEMKNPITNMFNLKYNRYRPVPTQWENVPEDTA 271
 QY 161 DYRKFRSLPSVDGQKRTFRVRSRFPPLCGSAQHSEMS 219
 DB 272 SHRDSFTLQDILLPNTVEVSIKCIHKDGHG---FWSQMS 307

RESULT 12
 ID 097597 PRELIMINARY; PRT; 349 AA.
 AC 097597;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN (FRAGMENT).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 PP SEQUENCE FROM N.A.
 PR MEDLINE=20080132; PubMed=10614495;
 RA Triglona W.L., Brown W.C., Estes D.M.;
 RT "Functional implications for signaling via the IL4R/IL13R complex on
 RT bovine cells.";
 RL Vet. Immunol. Immunopathol. 72:73-79(1999).
 DR EMBL: AF074402; AAC98147.1; -.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003532; Hematopo_receptor_S_F2.
 DR PROSITE: PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
 RN Receptor.
 FT NON_TER 1 1
 FT NON_TER 349 349
 FT SEQUENCE 349 AA; 39644 MW; D61A4C918B1940A6 CRC64;

Query Match 10.6%; Score 137; DB 6; Length 349;
 Best Local Similarity 24.0%; Pred. No. 4.1e-05;
 Matches 52; Conservative 37; Mismatches 98; Indels 30; Gaps 11;

QY 38 VOCEFYFVNEVMCTN---NSSSEPOPTNLTHYWKNSNDKVKCKSH-YLFSEELTSG 92
 DB 98 LQCIWHNLRYMKCTWLPERNASDPD---NYLLYVHNSL--GRILQENYRGGHIAQS 152
 QY 93 CQLOKKEIHLVQTYVQ--LQDPREPRKQATQMLKLNLYIPWAPENLTLLKLSQLEL 150
 DB 153 FNLTKVKNSSEHSHSVQVMDNAGKISPSFNIVPLTSHVKP--DPSHIKMLSFQNGDLVY 211
 QY 151 MNWN--RFLNHCL-----EHLVQYRTDMDHSWTE-----QSDVYRHK-----FSLPSVDQ 194
 DB 212 QNTNQNQNSQCLQEVYEVINSHAFETIDIFYEAKQKQNTPEFEGLEGITCFMVPGLPD 271
 QY 195 KRYTFVRSRFPNPLC-GSAQHSEMSHPIMHWSNTSK 230
 DB 272 TLNTVYRIVKTNKLCYEDDKLMSNWSQAMSIGOKANQ 308
 RESULT 13
 ID 064146 PRELIMINARY; PRT; 896 AA.
 AC 064146;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95370942; PubMed=7643220;
 RA Appel K., Buttini M., Sauter A., Gebicke-Haerter P.J.;
 RT "Cloning of rat interleukin-3 receptor beta-subunit from cultured
 RL microglia and its mRNA expression in vivo."; J. Neurosci. 15:5800-5809(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WISTAR; TISSUE=BRAIN;
 RA Gebicke-Haerter P.J.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: S79283; A035068.1; -
 DR EMBL: A2000555; CA04186.1; -
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR00282; CytoK_receptor_2.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003531; Hematopo_receptor_S_F1.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 2.
 PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
 Signal.
 NON_TER 1
 FT SEQUENCE 896 AA; 99504 MW; 4C6E3B288A4A1052 CRC64;
 SQ SEQUENCE 896 AA; 99504 MW; 4C6E3B288A4A1052 CRC64;

Query Match 10.6%; Score 136.5; DB 11; Length 896;
 Best Local Similarity 23.9%; Pred. No. 0.00014;
 Matches 48; Conservative 41; Mismatches 83; Indels 29; Gaps 11;
 QY 38 VOCFENVYVNMCTWNSSEPOPTNLTLHYWKNSDNDKVKCSHYLFSEITSG----- 92
 DB 251 LQCFEGIOSLSCSNHWMTK-VTDSVSFGLFYSSSPKAGEKKCSYV--KELQASRYTRY 307
 QY 93 -COLQKEITHLYQTFTVVOLODPRPRROATQMLKQNLVTPWAPENLTILKLSQELN 151
 DB 308 HCSLNVSDPAHSAQYTVSK-----RLQGRKIESFN-HIMNPPTLTLNTRNS-VSLH 360
 QY 152 MNRR-----FLNHCLEHLVQYRTD--MDHSWTEQSDVRYRKFSLPSVQGRYTFYRYS 203
 DB 361 METQKMSYFIFQIAFO--VQYKKKIDRWEDSKTE-NLHAHSMOLPQLEPSTICARVY 417
 QY 204 RNPPLGSAQHWSEWSHPITW 224
 DB 418 KTIPEYKGL--WSEWSNNECTW 436

RESULT 14
 5R3
 Q9H5R3 PRELIMINARY; PRT; 232 AA.
 Q9H5R3;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CDNA: FLJ23147 FIS, CLONE LMG09295.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RA Kawakami T., Nouguchi S., Itoh T., Shigetani K., Senba T., Matsumura K.,
 RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
 RA Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y., Ota T., Suzuki Y.,
 RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
 RA Iisaka T., Sugano S.;
 RT "NEO human cDNA sequencing project";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK028800; BAB15557.1; -
 SQ SEQUENCE 232 AA; 26703 MW; 56946BE74C226F5 CRC64;

Query Match 10.6%; Score 136; DB 4; Length 232;
 Best Local Similarity 23.1%; Pred. No. 3.2e-05;
 Matches 55; Conservative 33; Mismatches 54; Indels 96; Gaps 13;
 QY 37 EVOCFENVYVNMCTWNSSEPOPTNLTLHYWKNSDNDKVKCSHYLFSEITSGCOL- 95
 DB 30 QIOIIVFNLETQVTVWNAKSKSR-TNLTFHYRF-NGD-EAYDQCTNYLLOGGHTSGCLLD 86
 QY 96 -OKKEITHLY-----QTFVVOLODPRPRROATQMLKQNLVTPWAPENLTILH 141
 DB 87 AEGRDILVFSTRNGTHPVFTASRMWVYLLKPSRK-----HYRFSWHDQAVTV- 135
 QY 142 KLSQSELELNMNNRFLNHCLEHLVQYRTDWSWTEQ----- 178
 DB 136 ---TCSDSLSTGSD-----LLYEVOYRSPFDTEMQTSKSYTQACVQWCDLCLQSPPR 185
 QY 179 -----SVDYRH-----KESLPVSDGOKRYTFYRSRFPNLGSAQHWSEWS 219
 DB 186 KRFPSCLSLPSSWDYRHPRLANFCIISRDC-----VSP-C-----WPGWS 226

RESULT 15
 09IBF6
 ID 09IBF6 PRELIMINARY; PRT; 611 AA.
 AC 09IBF6;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PROLACTIN RECEPTOR.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxId=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20289252; PubMed=10830440;
 RA Yamamoto T., Nakayama Y., Abe S.-I., Kawahara A.;
 RT "Cloning of cDNA for Xenopus prolactin receptor and its metamorphic
 RL dev. growth differ. 42:167-174(2000).
 DR EMBL: AB030443; BA090400.1; -
 DR HSSP: P16471; 1BP3.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003528; Hematopo_receptor_L_F1.
 DR Pfam: PF00041; fn3; 1.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
 KW receptor.
 SQ SEQUENCE 611 AA; 68315 MW; 7E0DF76F21D8CE97 CRC64;

Query Match 10.1%; Score 130; DB 13; Length 611;
 Best Local Similarity 24.7%; Pred. No. 0.00037;
 Matches 59; Conservative 36; Mismatches 100; Indels 44; Gaps 13;
 QY 2 NTFTLPNGNEDTADFTLTPPTDSLVSITPLPEV--QCFVNVYVNMCTWNSSE-P 58
 DB 4 NLAPTP-----SVAVTFLFTLYVSLNAOSLPGRVIDIKCRSEKRYEFSQWKKGSOGG 58
 QY 59 OPTNLTLHYWKNSDNDKVKCSHYLFSEITSG--COLQKE-----IHLVQTFVVO 109
 DB 59 LPTNYSI--LYRKENDPKITECPDY-----VTSGLNSCFPDKAHNSFYTHIY--VN 107
 QY 110 LODPRPRROATQMLKQNLVTPWAPENLTILH-KLSQSELELNM-----NNRFLNHC 160
 DB 108 ATNALGSNVSDSESVPTTYIVQYPTPTNVSIAVESGHHDLKMLPRAWVQSGMLT-- 165
 QY 161 LEHLVQYRTDWSWTEQSDVRYRKFSLPSVQGRYTFYRYSRNPPLGSAQHWSEWS 219
 DB 166 LKYEVRKEKEQEWENALVGNQLKRLGLTTPGGNVVQVRC--PDSG--HWSEWS 219

Fri, Jun 28 07:58:59 2002

us-09-825-561a-4.rspt

Page 7

Search completed: June 28, 2002, 07:44:30
Job time: 225 sec

Fri Jun 28 07:58:59 2002

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:46:27 ; Search time 110.69 Seconds

(without alignments)
218.756 Million cell updates/sec

Title: US-09-825-561A-6

Perfect score: 1195

Sequence: 1 CPDLVCYTDVLTQVICILEM.....SDPVIRQTSSEIKESGMNH 218

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Gapop 10.0 , Gapect 0.5

rched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1195	100.0	289	21	AAV45029
2	1195	100.0	361	21	AAV69883
3	1195	100.0	538	20	AAV27450
4	1195	100.0	538	21	AAAB18634
5	1195	100.0	538	21	AAV79312
6	1195	100.0	538	21	AAV45031
7	1195	100.0	538	22	AAAB69886
8	1195	100.0	538	22	AAAB48001
9	1195	100.0	606	21	AAAB18629
10	1195	100.0	606	21	AAV79316
11	1188	99.4	538	21	AAV94304

12	1188	99.4	538	22	AAU08728
13	1187	99.3	471	21	AAV45030
14	1170	97.9	538	22	AAE02459
15	1159	97.0	538	21	AAV69888
16	1145	95.8	460	21	AAV69890
17	1138	95.2	375	21	AAV69889
18	1077	90.1	568	21	AAV94305
19	1077	90.1	568	22	AAU08729
20	1077	90.1	568	22	AAE02457
21	844	70.6	529	21	AAV79320
22	838	70.1	529	22	AAAB48002
23	548	45.9	158	21	AAV69891
24	543.5	45.5	144	21	AAV69884
25	521.5	43.6	144	21	AAV69887
26	400	33.5	397	21	AAV79319
27	362	30.3	227	21	AAV69885
28	176	14.7	57	22	AB539255
29	176	14.7	57	22	AB524090
30	176	14.7	57	22	AAV59919
31	176	14.7	57	22	AAV72513
32	176	14.7	57	22	AAV19611
33	176	14.7	57	22	AAV32757
34	148	12.4	878	17	AAV92529
35	145	12.1	576	16	AAV78613
36	145	12.1	592	17	AAV92527
37	145	12.1	596	16	AAV78610
38	145	12.1	600	16	AAV78610
39	145	12.1	600	17	AAV92526
40	145	12.1	878	16	AAV78608
41	144.5	12.1	539	11	AAV06647
42	144	12.1	783	18	AAV24054
43	144	12.1	805	18	AAV22106
44	144	12.1	842	18	AAV22102
45	144	12.1	894	18	AAV24064

ALIGNMENTS

RESULT	1
AAV45029	standard; Protein; 289 AA.
XX	
AC	AAV45029;
XX	
DT	31-MAY-2000 (first entry)
XX	
DE	HUMAN Orphan Cytokine Receptor-10 (OCRI0) polypeptide.
XX	
KW	Human; Orphan Cytokine Receptor-10; OCRI0; chromosome 16p12;
KW	cytokine; screen; cognate ligand; treatment; endocrine disorder;
XX	
XX	immune disorder.
OS	Homo sapiens.
XX	
FH	Key
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FT	Domain
FT	122..123
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FT	118..169
FT	/label= Mature_HUMAN_OCRI0
FT	238..255
FT	/label= Proline_hinge_motif
FT	263..278
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FT	/note= "Putative and hydrophobic"
XX	
XX	/label= "jak-binding_region"
XX	/note= "potential"
XX	
XX	W0200008152-A1.

Human HNOVIR poly
HUMAN OCRI0-Fc fus
Human DNAX cytokin
Mouse haemopoietin
Human NR8alpha/IgG
Human NR8alpha/TP0
Human HNOVIR poly
Human HNOVIR poly
Human DNAX cytokin
Mouse cytokine rec
Murine IL-9/IL-2 r
Human NR8beta/FLAG
Human haemopoietin
Mouse haemopoietin
Mouse cytokine rec
Human haemopoietin
Peptide #6761 enco
Protein #6089 enco
Human brain expres
Human bone marrow
Peptide #6045 enco
Peptide #6794 enco
Fas sequence from
Expression vector
Fas antigen #2. S
Expression vector
Expression vector
Fas antigen #1. S
Murine IL-3 recept
Murine interleukin
Murine WSK recepto
Murine leptin rece
Murine leptin rece
Murine WSK recepto

PD 17-FEB-2000.
 XX
 PF 16-JUL-1999; 99WO-US16060.
 XX
 PR 04-AUG-1998; 98US-0128820.
 XX
 PA (REGC-) REGENERON PHARM INC.
 XX
 PI Maslakowski PJ, Morris J, Valenzuela DM;
 XX
 DR WPI; 2000-205707/18.
 DR N-PSDB; AA250746.
 XX
 PT New HUMAN orphan cytokine receptors 10 and 10-A useful for screening
 PT for drugs e.g. receptor agonists that may mediate survival and
 PT differentiation in cells naturally expressing the receptor and for
 PT screening for cognate ligands
 XX
 PS Example 1; Page 21; 54pp; English.
 CC The present sequence is the HUMAN Orphan Cytokine Receptor-10
 CC (OCRI10) polypeptide. HUMAN OCRI10 gene is located on chromosome 16p12.
 CC It is expressed at high levels in spleen, thymus, peripheral blood
 CC leucocytes and lymph nodes and moderately in heart and placenta. It
 CC has a role in immune system and cytokine function. It is useful in
 CC screening for cognate ligands or drugs that mediate survival and
 CC differentiation of cells expressing this receptor. Modified HUMAN
 CC OCRI10 or its agonist can be used in the treatment of endocrine or
 CC immune disorders.
 XX
 SQ Sequence 289 AA:
 Query Match 100.0%; Score 1195; DB 21; Length 289;
 Best Local Similarity 100.0%; Pred. No. 6.4e-116;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPDLVCTDYLYQIVYICILEMNNLHPSTLTLTWQDYELKDEATSCSLHRSANHTATY 60
 DB 20 cpdlvcytdylyqivcilemnnlhpsltltwtqdyeelkdeatcslhrsahnatthy 79
 QY 61 TCHMDVHFHMADDFISVNTDQSGNYSOECGSFLAESIKRAPPFNTVTFSGQYNISMR 120
 DB 80 tchmdvrfhmaddfisvntdsgnysqecgsflaesikrappfnvtvtfsgqyniswr 139
 QY 121 SDYEDPAFYMLKGLQYELQYRNNGDPWAVSPRRKLISVDSRSVSLPLEFRKDSYELQ 180
 DB 140 sdyedpafymkglqyelqyrnngdpwavsprkklisvdsrsvslplefrkdsyelyq 199
 DB 181 VRAGPMGSSYOGTMSWSDPVIRFOTQSEELKEGMNPH 218
 200 vragpmpgssyogtmswspdvlirfqseelkegmnp 237
 RESULT 2
 AAY69883
 ID AAY69883 standard; Protein; 361 AA.
 XX
 AC AAY69883;
 XX
 DT 24-MAY-2000 (first entry)
 XX
 DE Human haemopoietin receptor family member NR8alpha.
 XX
 KW Haemopoietin receptor family; NR8; antibody; diagnosis;
 KW blood formation disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO9967290-A1.
 XX
 PD 29-DEC-1999.
 XX

PF 23-JUN-1999; 99WO-JP03351.
 XX
 PR 24-JUN-1998; 98JP-0214720.
 PR 19-OCT-1998; 98JP-0237409.
 XX
 PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
 XX
 PI Nomura H, Maeda M;
 XX
 DR WPI; 2000-116933/10.
 DR N-PSDB; AA259237.
 XX
 PT Hemopoietin receptor protein family NR8 used for diagnosis of blood
 PT formation disorders -
 XX
 PS Claim 1; Fig 5-6; 176pp; Japanese.
 CC This sequence represents a novel haemopoietin receptor protein family
 CC NR8, designated NR8alpha. Antibodies to the NR8 family proteins are used
 CC for the diagnosis of blood formation disorders. Compounds identified as
 CC binding to the proteins are used for the treatment of such disorders.
 XX
 SQ Sequence 361 AA:
 Query Match 100.0%; Score 1195; DB 21; Length 361;
 Best Local Similarity 100.0%; Pred. No. 8.8e-116;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPDLVCTDYLYQIVYICILEMNNLHPSTLTLTWQDYELKDEATSCSLHRSANHTATY 60
 DB 20 cpdlvcytdylyqivcilemnnlhpsltltwtqdyeelkdeatcslhrsahnatthy 79
 QY 61 TCHMDVHFHMADDFISVNTDQSGNYSOECGSFLAESIKRAPPFNTVTFSGQYNISMR 120
 DB 80 tchmdvrfhmaddfisvntdsgnysqecgsflaesikrappfnvtvtfsgqyniswr 139
 QY 121 SDYEDPAFYMLKGLQYELQYRNNGDPWAVSPRRKLISVDSRSVSLPLEFRKDSYELQ 180
 DB 140 sdyedpafymkglqyelqyrnngdpwavsprkklisvdsrsvslplefrkdsyelyq 199
 QY 181 VRAGPMGSSYOGTMSWSDPVIRFOTQSEELKEGMNPH 218
 DB 200 vragpmpgssyogtmswspdvlirfqseelkegmnp 237
 RESULT 3
 AAY27450
 ID AAY27450 standard; Protein; 538 AA.
 XX
 AC AAY27450;
 XX
 DT 26-NOV-1999 (first entry)
 XX
 DE Human MU-1 haematopoietin receptor protein.
 XX
 KW MU-1 haematopoietin receptor protein; gene therapy;
 KW cell proliferation; cytokine production; immune response; cancer;
 KW autoimmune disease; transplant rejection; haematopoiesis; anemia;
 KW gene mapping; nutritional supplement; human.
 XX
 OS Homo sapiens.
 XX
 PN WO9947675-A1.
 XX
 PD 23-SEP-1999.
 XX
 PF 17-MAR-1999; 99WO-US05854.
 XX
 PR 17-MAR-1998; 98US-0040005.
 XX
 PA (GEMY) GENETICS INST INC.
 XX

PI Donaldson D, Ungar M;
XX WPI: 1999-562115/47.
DR N-PSDB; AA207535.
XX
PT New nucleic acid encoding the MU-1 hematopoietin receptor protein, used
PT for treating e.g. cancer, autoimmune disease or abnormal hematopoiesis
PI
XX
PS Claim 9; Page 33-35; 37pp; English.
XX
CC This represents a MU-1 hematopoietin receptor protein. The protein can
CC be produced by standard recombinant methodology. The MU-1 protein has the
CC biological activity of the MU-1 hematopoietin receptor superfamily chain.
CC It is used to screen for specific binding agents; to raise specific
CC antibodies; as assay reagents, tissue markers etc. and therapeutically
CC (optionally) expressed from the MU-1 gene by gene therapy). Many possible
CC activities/uses of the MU-1 protein are described without supporting
CC evidence, e.g. they regulate cell proliferation and differentiation,
CC induce production of cytokines, stimulate or suppress an immune response
CC (e.g. for treating immune deficiency of any etiology, cancer or
CC autoimmune disease, and for preventing transplant rejection) and regulate
CC of hematopoiesis, e.g. for treating anemia. The MU-1 gene is used as a
CC research reagent, for recombinant production of the protein, as tissue or
CC molecular weight marker, for gene mapping; for production of anti-DNA or
CC anti-protein antibodies etc. The MU-1 protein and the nucleic acids are
CC also useful as nutritional supplements or sources and the antibodies can
CC be used therapeutically, as assay reagents and for affinity purification.
XX
SQ Sequence 538 AA;
Query Match 100.0%; Score 1195; DB 20; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.6e-115; Indels 0; Gaps 0;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CPDLVCYTDYLTQVTCILEMMNLHPSTLTLTWQDOYEELKDEATCSLHRSANATHATY 60
DB 20 cpdlvcytdyldqvticllemmnlhpsltltltwqdyeelkdeatcslnhsanathaty 79
QY 61 TCHMDVFNHMAADIFSVNITDQSGNYSQECGFLAESIKPAPPNVYTFPSQYINISMR 120
DB 80 tchmdvfnhmadifsvnitdsgnysqecgsflaesikpappnvtytfpsqyniswr 139
QY 121 SDYEDPAFMYMKGKLOYELQYRNRPWAVSPRRKLISVDSRSVSLPLEFRDSSYELO 180
DB 140 sdyedpafmylkgkloyelqyrnrgpavsprrklisvdsrsvsllplefrkssyelo 199
QY 181 VRAGPMGSSYOGTWSWSDPVIFOTOSSELKEGNMNP 218
DB 200 vragpmpgssyogtwsesdvpvifotoseelkegnmnp 237
RESULT 4
AA18634
ID AA18634 standard; Protein; 538 AA.
XX
AC AA18634;
XX
DT 22-JAN-2001 (first entry)
XX
DE A human zalphal1 ligand polypeptide.
XX
KM zalphal1 ligand; cytokine; haematopoietic cell proliferation; lymphoma;
KM tumorigenesis; leukaemia; hematopoiesis; B cell tumour.
XX
OS Homo sapiens.
XX
PN WO200053761-AZ.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000MO-US06067.

XX 09-MAR-1999; 99US-0264908.
PR 11-MAR-1999; 99US-0265992.
PR 01-JUL-1999; 99US-0142013.
XX
PA (ZYMO) ZYMOGENETICS INC.
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA;
PI Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX WPI: 2000-565600/52.
DR N-PSDB; AAA75557.
XX
PT New human cytokine, designated zalphal1 ligand, useful for stimulating
PT the proliferation and/or development of haematopoietic cells in vitro
PT and in vivo, and for treating tumorigenesis -
XX
PS Disclosure; Page 255-256; 256pp; English.
XX
CC The present sequence represents a human zalphal1 ligand polypeptide,
CC which is a cytokine. The zalphal1 ligand is useful for stimulating the
CC proliferation and development of haematopoietic cells in vitro and in
CC vivo. Zalphal1 ligand polynucleotides can be used as primers or probes
CC for cloning the zalphal1 gene. The zalphal1 ligand is useful for
CC treating tumorigenesis. A zalphal1 ligand-saporin fusion toxin may be
CC used for treating leukemias and lymphomas. Antagonists against zalphal1
CC ligand are useful as research reagents for characterizing ligand-receptor
CC interaction. Antagonists are also useful for inhibiting expansion,
CC proliferation, activation and differentiation of cells involved in
CC regulating hematopoiesis. The zalphal1 ligand may also be used to
CC stimulate an immune response against B cell tumour, a virus, a parasite
CC or a bacterium. The zalphal1 polypeptides, polynucleotides, antagonists,
CC agonists and antibodies are also useful for the detection, diagnosis,
CC prevention, and treatment of diseases associated with a zalphal1 ligand
CC genetic defect.
XX
SQ Sequence 538 AA;
Query Match 100.0%; Score 1195; DB 21; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.6e-115; Indels 0; Gaps 0;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CPDLVCYTDYLTQVTCILEMMNLHPSTLTLTWQDOYEELKDEATCSLHRSANATHATY 60
DB 20 cpdlvcytdyldqvticllemmnlhpsltltltwqdyeelkdeatcslnhsanathaty 79
QY 61 TCHMDVFNHMAADIFSVNITDQSGNYSQECGFLAESIKPAPPNVYTFPSQYINISMR 120
DB 80 tchmdvfnhmadifsvnitdsgnysqecgsflaesikpappnvtytfpsqyniswr 139
QY 121 SDYEDPAFMYMKGKLOYELQYRNRPWAVSPRRKLISVDSRSVSLPLEFRDSSYELO 180
DB 140 sdyedpafmylkgkloyelqyrnrgpavsprrklisvdsrsvsllplefrkssyelo 199
QY 181 VRAGPMGSSYOGTWSWSDPVIFOTOSSELKEGNMNP 218
DB 200 vragpmpgssyogtwsesdvpvifotoseelkegnmnp 237
RESULT 5
AA79312
ID AA79312 standard; Protein; 538 AA.
XX
AC AA79312;
XX
DT 18-JUL-2000 (first entry)
XX
DE Human cytokine receptor zalphal1.
XX
KM Cytokine receptor; zalphal1; human; chromosome 16p11.1;
KM apoptosis; signal transduction; growth factor; cancer; tumour;
KM infection; immunosuppressive; immunostimulant; autoimmune disease;

KM Leukemia; lymphoma; transplant rejection; therapy; diagnosis.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /note= "signal peptide"
 FT /note= "mature protein: a polypeptide comprising the mature protein is specifically claimed in Claim 27(d)"
 FT Region 214..218
 FT /note= "MSXMS motif"
 FT Domain 20..237
 FT /note= "cytokine-binding domain: a polypeptide comprising this domain is specifically claimed in Claim 27(a)"
 FT Domain 192..202
 FT /note= "penultimate strand region"
 FT Domain 238..255
 FT /note= "transmembrane domain"
 FT Domain 256..538
 FT /note= "intracellular signalling domain: a polypeptide comprising this domain is specifically claimed in Claim 27(c)"
 FT Region 267..273
 FT /note= "Box I signalling site"
 FT Region 301..304
 FT /note= "Box II signalling site"
 XX WO200017235-A2.
 PD 30-MAR-2000.
 XX 23-SEP-1999; 99WO-US22149.
 XX 23-SEP-1998; 98US-0159254.
 PR 09-MAR-1999; 99US-0265117.
 PR 06-JUL-1999; 99US-0347930.
 XX (ZYMO) ZYMOGENETICS INC.
 PA Presnell SR, Conklin DC, Novak JE, Hammond AK;
 PI WPI, 2000-292825/25.
 DR N-PSDB: AA294533, AA294534.
 XX Novel nucleic acid encoding zaiphal1 polypeptide, useful for treating e.g. viral infection or tumors, and for identifying ligands that stimulate cell proliferation -
 PT Claim 27(e); Page 148-149; 190pp; English.
 XX The present sequence is that of zaiphal1, a novel human class I CC cytokine receptor that may be involved in an apoptotic cellular CC pathway, or is a cell-cell signalling molecule, growth factor CC receptor, or extracellular matrix associated protein with growth CC factor hormone activity. The sequence was deduced from a cDNA clone CC (see AA294533) isolated from a spinal cord library. Polypeptides CC comprising amino acids 20-237, 20-255, 256-538, 20-538 and 1-538 of CC the present sequence are claimed. zaiphal1 is expressed in lymph CC node, peripheral blood leucocytes, spleen and thymus. The mRNA is CC also abundant in the Raji cell line (ATCC CCL 86) derived from CC Burkitt's lymphoma. Zaiphal1 polypeptides, and fusion proteins CC including them, can be obtained by expression in recombinant host CC cells. They are used to detect ligands (also ligand agonists and CC antagonists) that stimulate proliferation and/or development of CC haematopoietic, lymphoid and myeloid cells, in vitro or in vivo, CC e.g. as a replacement for serum in culture media; in soluble form CC to block ligand activity (direct antagonists) and to detect CC ligand-expressing cancers; to raise specific antibodies; and for CC purification of cognate ligands. Agonistic ligands may stimulate CC cell-mediated immunity, e.g. for treating (viral) infections

CC associated with immunosuppression, improving the activity of
 CC vaccines, suppressing tumours, treating leukaemia and improving
 CC T-cell regeneration after bone marrow transplant. Antagonists are
 CC useful as immunosuppressants, e.g. in the treatment of autoimmune
 CC disease (e.g. rheumatoid arthritis, multiple sclerosis, diabetes),
 CC to prevent transplant rejection and to treat T-cell leukemia or
 CC lymphoma.
 XX Sequence 538 AA;
 SQ
 Query Match 100.0%; Score 1195; DB 21; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.6e-115;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CPDLVGYTDYLYQTYCTLEMMNHLPSLTLTWQOYELKDEATSCSLHSANHATATY 60
 DB |||||||
 DB 20 cpdlvgytdylyqtyctlemmnlhpsltltwqdyeeldeatscslhsanhataty 79
 QY 61 TCHMDVPHFMADIFSVNITDQSGNYSQEGSFLLAESIKPAPFNTVTFSGQYNTSMR 120
 DB |||||||
 DB 80 tchmdvfhmddlfsvnltdqsgnysqegsfllaesikpappfnvtvtfsgqynlswr 139
 QY 121 SDYEDPAFYMLKGLQYELQYRNKGDPWAVSPRRKLISVDSRVSLLPLEFRKDSYELQ 180
 DB |||||||
 DB 140 sdyedpatfymkglqyelyrnkgdpwavsprkrlisvdsrsvllplefrkdsyelyq 199
 QY 181 VRAGPMGSSYQGTWSEMSDPVITFOTQSEELKEGMNH 218
 DB |||||||
 DB 200 vragpmgssyqgtwsemsdpvitfqseelkegmnh 237
 RESULT 6
 AAY45031
 ID AAY45031 standard; Protein: 538 AA.
 XX
 AC AAY45031;
 XX
 DT 31-MAY-2000 (first entry)
 XX
 DE HUMAN Orphan Cytokine Receptor 10 (OCR10)-A polypeptide.
 XX
 KM Human; Orphan Cytokine Receptor 10-A; OCR10-A; cytokine; screen;
 KM cognate ligand; treatment; endocrine disorder; immune disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200008152-A1.
 PD 17-FEB-2000.
 XX
 XX 16-JUL-1999; 99WO-US16060.
 XX
 PR 04-AUG-1998; 98US-0128820.
 XX
 PA (REGF-) REGENERON PHARM INC.
 XX
 PI Maslakowski PJ, Morris J, Valenzuela DM;
 DR WPI: 2000-205707/18.
 DR N-PSDB: AA250748.
 XX
 XX New HUMAN orphan cytokine receptors 10 and 10-A useful for screening
 PT for drugs e.g. receptor agonists that may mediate survival and
 PT differentiation in cells naturally expressing the receptor and for
 PT screening for cognate ligands
 XX
 PS Example 10; Page 39-41; 54pp; English.
 XX The present sequence is that of HUMAN Orphan Cytokine Receptor 10-A
 CC (OCR10-A) polypeptide. It is expressed at high levels in spleen, thymus,
 CC peripheral blood leucocytes and lymph nodes and moderately in heart and
 CC placenta. It has a role in immune system and cytokine function. It is

CC useful in screening for cognate ligands or drugs that mediate survival
CC and differentiation of cells expressing this receptor. Modified HUMAN
CC OCRI0-A or its agonist can be used in the treatment of endocrine or
CC immune disorders.
XX
SQ Sequence 538 AA;

Query Match 100.0%; Score 1195; DB 21; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.6e-115;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCTDYLGTVICILEMWNLPSTLTITWODYEELKDEATSCSLRSANHTATY 60
Db 20 cpdlvctdylgvlicilemwnlpstltitwqdyeelkdeatscslrsanhtat 79
QY 61 TCHMDVFHMADDFSVNITDQSGNSQECGSFLAESIKPAPPNVTVTFSGQYNISM 120
80 tchmdvfhmaddifsvnitdsgnsgcgcsflaesikpappfnvtfvtfsgqynism 139
QY 121 SDYEDPAFYMLKGLQYELQYRNKGPMAVSPRRKLISVDSVSLPLEFRKDSSEYELQ 180
Db 140 sdyedpafymkglqyelqyrngdpwvsprrklisvdsrsvslplefrkdsseyelq 199
QY 181 VRAGPMGSSYOGTSEMSDPVIFQTQSEELKEGMNPH 218
Db 200 vragpmpgssyogtsemsdpvifqtqseelkegmnp 237

RESULT 7

AA69886
ID AAY69886 standard; Protein; 538 AA.

AC AAY69886;

DT 24-MAY-2000 (first entry)

XX Human haemopoietin receptor family member NR8gamma.

KM Haemopoietin receptor family; NR8; antibody; diagnosis;

KW blood formation disorder.

XX Homo sapiens.

XX WO967290-A1.

XX 29-DEC-1999.

XX 23-JUN-1999; 99WO-JP03351.

XX 24-JUN-1998; 98JP-0214720.

XX 19-OCT-1998; 98JP-0297409.

PA (CHUGAI) CHUGAI RES INST MOLECULAR MEDICINE INC.

PI Nomura H, Maeda M;

XX WPI: 2000-116933/10.

DR N-PSDB; AAZ59240.

PT Homopoleitin receptor protein family NR8 used for diagnosis of blood

PT formation disorders -

PS Claim 4; Fig 9-10; 176pp; Japanese.

XX This sequence represents a novel haemopoietin receptor protein family

CC NR8, designated NR8gamma. Antibodies to the NR8 family proteins are used

CC for the diagnosis of blood formation disorders. Compounds identified as

CC binding to the proteins are used for the treatment of such disorders.

XX Sequence 538 AA;

Query Match 100.0%; Score 1195; DB 21; Length 538;
Best Local Similarity 100.0%; Pred. No. 1.6e-115;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCTDYLGTVICILEMWNLPSTLTITWODYEELKDEATSCSLRSANHTATY 60
Db 20 cpdlvctdylgvlicilemwnlpstltitwqdyeelkdeatscslrsanhtat 79
QY 61 TCHMDVFHMADDFSVNITDQSGNSQECGSFLAESIKPAPPNVTVTFSGQYNISM 120
Db 80 tchmdvfhmaddifsvnitdsgnsgcgcsflaesikpappfnvtfvtfsgqynism 139
QY 121 SDYEDPAFYMLKGLQYELQYRNKGPMAVSPRRKLISVDSVSLPLEFRKDSSEYELQ 180
Db 140 sdyedpafymkglqyelqyrngdpwvsprrklisvdsrsvslplefrkdsseyelq 199
QY 181 VRAGPMGSSYOGTSEMSDPVIFQTQSEELKEGMNPH 218
Db 200 vragpmpgssyogtsemsdpvifqtqseelkegmnp 237

RESULT 8

AAB48001
ID AAB48001 standard; Protein; 538 AA.

AC AAB48001;

DT 19-MAR-2001 (first entry)

XX Human IL-9/IL-2 receptor-like 16445 protein.

XX Interleukin-9; IL-9; IL-2 receptor; 16445 protein; inflammatory;

KW T-lymphocyte-related disorder; antiarthritic; antipsoriatic; human;

KW immunosuppressive; antiasthmatic; antiallergic; antithyroid; cytostatic;

KW antiarthritic; nephrotropic; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..19 /note="signal peptide"

FT Protein 20..538 /note="mature protein"

XX WO200069880-A1.

XX 23-NOV-2000.

XX 18-MAY-2000; 2000WO-US13687.

XX 18-MAY-1999; 99US-0313913.

PA (MILL-) MILLENNIUM PHARM INC.

PI Hodge MR;

XX WPI: 2001-016209/02.

DR N-PSDB; AAC84147.

PT Novel interleukin-9/interleukin-2 receptor-like polypeptides useful for

PT diagnosis and treatment immune, inflammatory and respiratory disorders

PT and in screening assays for identifying modulators -

XX Claim 8; Page 104-106; 119pp; English.

XX The invention relates to isolated human and murine interleukin-9 (IL-9)

CC /IL-2 receptor-like polypeptides. The plasmid containing the encoding

CC cDNA insert is deposited as ATCC PTA-350. The IL-9/IL-2 receptor-like

CC polypeptides (16445 proteins) can be recombinantly produced using

CC standard recombinant methodology. The 16445 proteins are used for

CC identifying their modulators and for diagnosis and treatment of immune,

CC inflammatory and respiratory disorders and disorders associated with

CC lungs, colon, kidney and lymphoid tissues including tonsil and thymus,

CC In particular T-lymphocyte-related disorders including atopic conditions
 CC such as asthma, allergy, rheumatoid arthritis, psoriasis, chronic
 CC inflammatory diseases and graft versus host disease, disorders involving
 CC the colon such as diarrhoea, dysentery, infectious enterocolitis, kidney
 CC disorders including polycystic kidney disease, cystic renal dysplasia,
 CC disorders of the thymus including lymphomas, Hodgkin disease and
 CC carcinoids. The 1643 polypeptides are also useful as modulating agents
 CC in antigen processes including growth promoting activity, particularly
 CC the antigen-independent proliferation of T-helper cell clones. The
 CC encoding nucleic acid is useful as primers or hybridization probes for
 CC the detection of IL-9/IL-2 receptor-like encoding nucleic acids and for
 CC tissue typing and in forensic biology. The present sequence represents
 CC the human IL-9/IL-2 receptor-like polypeptide (AAH16445).

XX
 SQ Sequence 538 AA;

Query Match 100.0%; Score 1195; DB 22; Length 538;
 Best Local Similarity 100.0%; Pred. No. 1.6e-115;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CPDLVCTDYLTQVTCILEMNNLHPSTLTLTWODYEELKDEATSCSLRSHAHNTHTATY 60
 |||||||
 Db 20 cpdlvctdyltqvtcilemnnlhpsltltltwgdqyeelkdeatscslrshahntathaty 79

QY 61 TCHMDVHFHMADDFSVNITDQSGNSOEGSFLAESIKPAPFVWVTFSGOYNISMR 120
 |||||||
 Db 80 tchmdvfhmaddfsvnltldqsgnysgecgstllaesikpaprlnvtvtisgqynisvr 139

QY 121 SDYEDPAFYMLKGLQYELQYRNKGDPMWVSPRRKLISVDSRSVSLPLEFRKDSSEYELQ 180
 |||||||
 Db 140 sdyedpafymkglqyelqyrnrgdpwvsprkllsvdsrsvsllplefrkdsseyelq 199

QY 181 VRAGPMGSSYOGTSEWSPVVFOTQSEELKEGMNPH 218
 |||||||
 Db 200 vragpmpgssyogtsewsdpvlfqtqseelkegmnp 237

RESULT 9
 AAB18629
 ID AAB18629 standard; Protein; 606 AA.

XX AAB18629;
 DT 22-JAN-2001 (first entry)

XX Amino acid sequence of MBP-human zalphall ligand fusion.
 DE zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;
 XX tumorigenesis; leukaemia; hematopoiesis; B cell tumour.
 KW

OS Synthetic.
 XX Homo sapiens.

PN WO200053761-A2.

PD 14-SEP-2000.

PF 09-MAR-2000; 2000WO-US06067.

PR 09-MAR-1999; 99US-0264908.

PR 11-MAR-1999; 99US-0265992.

PR 01-JUL-1999; 99US-0142013.

XX (ZYMO) ZYMOGENETICS INC.

XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA;
 PI Johnston JV, Nelson AJ, Dillon SR, Hammond AK;

DR WPI: 2000-565600/52.

DR N-PSDB; AAA75609.

XX New human cytokine, designated zalphall ligand, useful for stimulating

PT the proliferation and/or development of haematopoietic cells in vitro
 PT and in vivo, and for treating tumorigenesis -
 XX

PS Example 45; Page 245-247; 256pp; English.

XX The present sequence represents a MBP-human zalphall ligand fusion.
 CC zalphall ligand is a cytokine. The zalphall ligand is useful for
 CC stimulating the proliferation and development of haematopoietic cells
 CC in vitro and in vivo. zalphall ligand polynucleotides can be used as
 CC primers or probes for cloning the zalphall gene. The zalphall ligand
 CC is useful for treating tumorigenesis. A zalphall ligand-saporin fusion
 CC toxin may be used for treating leukaemias and lymphomas. Antagonists
 CC against zalphall ligand are useful as research reagents for
 CC characterizing ligand-receptor interaction. Antagonists are also useful
 CC for inhibiting expansion, proliferation, activation and differentiation
 CC of cells involved in regulating hematopoiesis. The zalphall ligand may
 CC also be used to stimulate an immune response against B cell tumour, a
 CC virus, a parasite or a bacterium. The zalphall polypeptides,
 CC polynucleotides, antagonists, agonists and antibodies are also useful
 CC for the detection, diagnosis, prognosis, prevention, and treatment of diseases
 CC associated with a zalphall ligand genetic defect.

XX Sequence 606 AA;

Query Match 100.0%; Score 1195; DB 21; Length 606;
 Best Local Similarity 100.0%; Pred. No. 1.9e-115;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCTDYLTQVTCILEMNNLHPSTLTLTWODYEELKDEATSCSLRSHAHNTHTATY 60
 |||||||
 Db 389 cpdlvctdyltqvtcilemnnlhpsltltltwgdqyeelkdeatscslrshahntathaty 448

QY 61 TCHMDVHFHMADDFSVNITDQSGNSOEGSFLAESIKPAPFVWVTFSGOYNISMR 120
 |||||||
 Db 449 tchmdvfhmaddfsvnltldqsgnysgecgstllaesikpaprlnvtvtisgqynisvr 508

QY 121 SDYEDPAFYMLKGLQYELQYRNKGDPMWVSPRRKLISVDSRSVSLPLEFRKDSSEYELQ 180
 |||||||
 Db 509 sdyedpafymkglqyelqyrnrgdpwvsprkllsvdsrsvsllplefrkdsseyelq 568

QY 181 VRAGPMGSSYOGTSEWSPVVFOTQSEELKEGMNPH 218
 |||||||
 Db 569 vragpmpgssyogtsewsdpvlfqtqseelkegmnp 606

RESULT 10
 AAY79316
 ID AAY79316 standard; Protein; 606 AA.

XX AAY79316;

DT 18-JUL-2000 (first entry)

DE Maltose binding protein-zalphall fusion protein.

XX Cytokine receptor; zalphall; maltose binding protein; human;
 KW apoptosis; signal transduction; growth factor; cancer; tumour;
 XX infection; gene therapy; diagnosis; huzalphall/MBP-6H.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Protein 1..386 /note="maltose binding protein"

FT Protein 389..606 /note="zalphall cytokine binding domain"

PN WO200017235-A2.

PD 30-MAR-2000.

PF 23-SEP-1999; 99WO-US22149.

XX 23-SEP-1998; 980S-0159254.
 PR 09-MAR-1999; 990S-0265117.
 PR 06-JUL-1999; 990S-0347930.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Presnell SR, Conklin DC, Novak JE, Hammond AK;
 DR WPI: 2000-292825/25.
 DR N-PSDB: AA294554.
 XX
 PT Novel nucleic acid encoding zalpahal polypeptide, useful for treating
 PT e.g. viral infection or tumors, and for identifying ligands that
 PT stimulate cell proliferation .
 XX
 PS Example 13; Page 166-168; 190pp; English.

XX The present sequence is that of a fusion protein, designated
 CC huZalpalhal1/MBP-6H, comprising a maltose binding protein (MBP)
 CC fused to the cytokine binding domain (amino acids 20-237) of
 CC human class I cytokine receptor zalpalhal1 (see AAY9312). An
 CC expression plasmid containing huZalpalhal1/MBP-6H DNA (see AA294554)
 CC was constructed via homologous recombination and the fusion protein
 CC was expressed in Escherichia coli BL21 using vector plasmid pTAP98.
 CC Zalpalhal1 may be involved in an apoptotic cellular pathway, or is a
 CC cell-cell signalling molecule, growth factor receptor, or
 CC extracellular matrix associated protein with growth factor hormone
 CC activity. The invention provides zalpalhal polypeptides (including
 CC fusion proteins), polynucleotides and antibodies, and methods for
 CC their use in the treatment and diagnosis of conditions associated
 CC with altered zalpalhal1 expression or activity.
 XX

SO Sequence 606 AA:

Query Match 100.0%; Score 1195; DB 21; Length 606;
 Best Local Similarity 100.0%; Pred. No. 1.9e-115;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CPDLVCTDYDLYQTVCILLEMNHLHPSTLTLTWODQYEELKDEATSCSLHRSANATHATY 60
 DB 389 CPDLVCTDYDLYQTVCILLEMNHLHPSTLTLTWQDYEELKDEATSCSLHRSANATHATY 448
 QY 61 TCHMDVHFHMADDFISVNTDQSGNYSOEGCSFLAESIKPAPFNVTYFSGQYINISWR 120
 DB 449 TCHMDVHFHMADDFISVNTDQSGNYSOEGCSFLAESIKPAPFNVTYFSGQYINISWR 508
 QY 121 SDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLPLEFRKDSSEYEQ 180
 DB 509 SDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLPLEFRKDSSEYEQ 568
 QY 181 VRAGPMGSSYOGTWSWSDPVIFOTQSEELKEGWNPH 218
 DB 569 VRAGPMGSSYOGTWSWSDPVIFOTQSEELKEGWNPH 606

RESULT 11
 AAAY94304
 ID AAY94304 standard; Protein: 538 AA.
 AC AAY94304;

XX 08-AUG-2000 (first entry)
 DE Human HNOVILR polypeptide 1.
 XX

KW Human: anticancer; anti-inflammatory; immunosuppressive; antiallergic;
 KW antiasthmatic; antirheumatic; antiarthritic; nootropic; vasotropic;
 KW neuroprotective; antibacterial; cerebroprotective; osteoprotic;
 KW nephrotropic; hepatotropic; hypotensive; hypertensive; antifungal;
 KW anti-HIV; antiprotozoal; antiviral; antianaemic; autoimmune disease;
 KW Crohn's disease; Alzheimer's disease; Parkinson's disease; stroke;

KW multiple sclerosis; cancer; infection; cardiovascular disease.

XX Homo sapiens.

XX WO200027882-A1.

XX 18-MAY-2000.

XX 01-NOV-1999; 99WO-US25617.

XX 06-NOV-1998; 98US-0187711.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Kikly KK, Michalovich D;

DR WPI: 2000-376497/32.

DR N-PSDB: AAA26984.

XX Claim 1; Page 30-31; 36pp; English.

XX The present sequence is a HNOVILR polypeptide which is believed to
 CC be a member of the cytokine receptor family of polypeptides. It shows
 CC homology with human interleukin receptor 2 and is therefore expected to
 CC have similar biological functions/properties. The polynucleotide may be
 CC obtained from a cDNA library derived from mRNA in cells of human bone
 CC marrow using expressed sequence tag (EST) analysis. Alternatively it
 CC may be obtained from natural sources such as genomic DNA libraries or
 CC can be synthesised using commercially available techniques. The growth,
 CC regulation and functional activities of cells are regulated through the
 CC interaction of cytokines and their cognate receptors. Thus the
 CC gene sequence and its product are useful for diagnosing or treating a
 CC wide range of diseases including cancer, inflammation, autoimmune
 CC disease, Crohn's disease, allergy, asthma, rheumatoid arthritis,
 CC Alzheimer's disease, Parkinson's disease, multiple sclerosis,
 CC head injury damage, septic shock, stroke, osteoporosis, osteoarthritis,
 CC cardiovascular disease, kidney disease, liver disease, ischemic injury,
 CC myocardial infarction, hypertension, hypertension, acquired immune
 CC deficiency syndrome (AIDS), male pattern baldness, and bacterial,
 CC fungal, protozoan and viral infections.
 XX

SO Sequence 538 AA:

Query Match 99.4%; Score 1188; DB 21; Length 538;
 Best Local Similarity 99.5%; Pred. No. 8.5e-115;
 Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CPDLVCTDYDLYQTVCILLEMNHLHPSTLTLTWODQYEELKDEATSCSLHRSANATHATY 60
 DB 20 CPDLVCTDYDLYQTVCILLEMNHLHPSTLTLTWQDYEELKDEATSCSLHRSANATHATY 79
 QY 61 TCHMDVHFHMADDFISVNTDQSGNYSOEGCSFLAESIKPAPFNVTYFSGQYINISWR 120
 DB 80 TCHMDVHFHMADDFISVNTDQSGNYSOEGCSFLAESIKPAPFNVTYFSGQYINISWR 139
 QY 121 SDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLPLEFRKDSSEYEQ 180
 DB 140 SDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLPLEFRKDSSEYEQ 199
 QY 181 VRAGPMGSSYOGTWSWSDPVIFOTQSEELKEGWNPH 218
 DB 200 VRAGPMGSSYOGTWSWSDPVIFOTQSEELKEGWNPH 237

RESULT 12
 AAU08728
 ID AAU08728 standard; Protein: 538 AA.
 AC AAU08728;

Query Match	99.4%	Score 1188	DB 22	Length 538
Best Local Similarity	99.5%	Pred. No. 8.5e-115		
Matches 217	Conservative 0	Mismatches 1	Indels 0	Gaps 0
1	CPDLYCCTPTDLYDTVCILMMNMLHPSSTLLTLMODQYEEELKDAETSSLSLRSAHNAHNTARY	60		
20	cpolyvcytdytlvticillemwnlhpstlltlwqdyeeelkdaetssllhrsamhachaty	79		
61	TCCHMDVFHMMADDFISVNTJTDOSGANSQCGSFFLAEASIKPAPFVNTVTFSGQVYISMR	120		
80	tchmdvfthmaddifsvnltjtdsgnysgcgcgffllaesikpappfnvntvtfsgqyismr	139		

121 SDTEDEAFYMLKGIQYELQYLRNRGDPMVAVSPRRKIISVDSRSVSLPLPEFRKDSYELQ 180

Query Match	Best Local Similarity	Score	DB	Length	471;
Matches 211; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;	

QY 1 CPDLVCTDYIQTVCILEMNLHPSTLTITWQOYEELKDEATSCSLHRSANATHARY 60
 Db 20 cpdlvctdyIqtvicilemnlhpsltltlwqdyeelkdeatscslhrsanathary 79
 QY 61 TCHMDVHFHMADDFSVNITDQSGNYSGCGSFLLAESIKPAPFNVTVFSGQYINSMR 120
 Db 80 tchmdvfhmaddfsvnitdsgnysgcgsfllaesikpappfnvtfvsgqynlsvr 139
 QY 121 SDYEDPAFYMLGKIQLEYQYRNKGDPMWASPRRKLISVDSRSVSLPLEFRKDSSEYEQ 180
 Db 140 sdyedpafymkgikleyqyrnrgdpmwvsprkklisvdsrsvsllplefrkdsseyeq 199
 QY 181 VRAGPMPGSSYOGTSEMSDPVIFOTQSEELKEGMNP 217
 Db 200 vragpmpgssyqgtsemsdpvifqtgseelkegmnp 236

SOURCE 14
 ID AAE02459 standard; Protein: 538 AA.
 AC AAE02459;
 XX 10-AUG-2001 (first entry)
 DE Human DNAX cytokine receptor subunit 3.2 (DCRS3.2).
 XX Human; immunomodulator; DNAX cytokine receptor subunit 3.2; DCRS3.2;
 KM therapy; immunological disorder; drug screening; cell development;
 XX chromosome 16p12; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /label= Signal_peptide 21..538
 FT /label= DCRS3.2
 FT /note= "Human mature DNAX cytokine receptor subunit 3.2"
 FT Misc-difference 108
 FT /note= "Encoded by GAN"
 FT Misc-difference 136
 FT /note= "Encoded by ATN"
 FT Misc-difference 199
 FT /note= "Encoded by CAN"

MO200136467-A2.
 XX 25-MAY-2001.
 PD 16-NOV-2000; 2000MO-0531363.
 PE 18-NOV-1999; 9905-0443060.
 PR 13-DEC-1999; 9905-0170320.
 XX (SCHE) SCHERING CORP.
 PA Gorman DM;
 XX PI
 DR WPI, 2001-343800/36.
 DR N-PSDB; AAD06412.
 XX New mammalian receptor proteins related to cytokine receptors, useful
 PT for regulating cell development and for diagnosis and treatment of
 PT immunological disorders -
 XX Claim 3; Page 16-17; 124pp; English.
 XX The present sequence is human DNAX cytokine receptor subunit 3.2
 CC (DCRS3.2) cDNA. DCRS3 gene is located on chromosome 16p12.
 CC Cytokine receptors, fragments and antibodies are useful for treating

CC immunological disorders. DCRS3 (50R), DCRS4 (cytor) or fragments are
 CC useful in drug screening to identify compounds having binding affinity
 CC to the receptor subunit. Modulators of DCRs are useful for modulating
 CC the physiology or development of a cell or tissue culture cells. A
 CC purified DCRS is useful as a reagent to detect antibodies generated in
 CC response to the presence of elevated levels of expression, or
 CC immunological disorders which lead to production of antibody to the
 CC endogenous receptor. Cytokine receptor sequences are useful as probes
 CC for detecting levels of the cytokine receptor in patients suspected of
 CC having an immunological disorder. Antibodies have therapeutic value, are
 CC useful as potent antagonists, in detecting or quantifying ligands, for
 CC isolating DCRs proteins and peptides, to screen expression libraries for
 CC particular expression products, to raise anti-idiotypic antibodies and
 CC for detecting or diagnosing various immunological conditions related to
 CC expression of the protein or cells which express the protein.

SQ Sequence 538 AA:
 QY 1 CPDLVCTDYIQTVCILEMNLHPSTLTITWQOYEELKDEATSCSLHRSANATHARY 60
 Db 20 cpdlvctdyIqtvicilemnlhpsltltlwqdyeelkdeatscslhrsanathary 79
 QY 61 TCHMDVHFHMADDFSVNITDQSGNYSGCGSFLLAESIKPAPFNVTVFSGQYINSMR 120
 Db 80 tchmdvfhmaddfsvnitdsgnysgcgsfllaesikpappfnvtfvsgqynlsvr 139
 QY 121 SDYEDPAFYMLGKIQLEYQYRNKGDPMWASPRRKLISVDSRSVSLPLEFRKDSSEYEQ 180
 Db 140 sdyedpafymkgikleyqyrnrgdpmwvsprkklisvdsrsvsllplefrkdsseyeq 199
 QY 181 VRAGPMPGSSYOGTSEMSDPVIFOTQSEELKEGMNP 218
 Db 200 vragpmpgssyqgtsemsdpvifqtgseelkegmnp 237

RESULT 15
 AAY69888
 ID AAY69888 standard; Protein: 538 AA.
 XX AAY69888;
 AC AAY69888;
 XX 24-MAY-2000 (first entry)
 DE Mouse haemopoietin receptor family member NR8gamma.
 XX Haemopoietin receptor family; NR8; antibody; diagnosis;
 KM blood formation disorder.
 XX Mus sp.
 OS WO9967290-A1.
 PN 29-DEC-1999.
 PD 23-JUN-1999; 99WO-JP03351.
 PE 24-JUN-1998; 98JP-0214720.
 PR 19-OCT-1998; 98JP-0297409.
 XX (CHUGAI) CHUGAI RES INST MOLECULAR MEDICINE INC.
 PA Nomura H, Maeda M;
 XX PI
 DR WPI, 2000-116933/10.
 DR N-PSDB; AAZ59242.
 XX Hemopoietin receptor protein family NR8 used for diagnosis of blood
 PT formation disorders -

XX Claim 6; Page 152-158; 176pp; Japanese.
 PS
 CC This sequence represents a mouse haemopoietin receptor protein family
 CC NR8, designated NR8gamma. Antibodies to the NR8 family proteins are used
 CC for the diagnosis of blood formation disorders. Compounds identified as
 CC binding to the proteins are used for the treatment of such disorders.
 XX
 SQ Sequence 538 AA;

Query Match 97.0%; Score 1159; DB 21; Length 538;
 Best Local Similarity 98.2%; Pred. No. 8.8e-112;
 Matches 214; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CPPLVGYTYLQTVTCILEMNNLHPSRTLLTWODQYELKDEATSCSLHRSANATHATY 60
 Db 20 cpplvcytdylqtvclilemwnlhpsrtlltwodqyaelkdeatcslhrsanhathaty 79
 QY 61 TCHMDVFRHMADDFISVNIITDQSGNYSQEGSFLAESIKRPAPFNVTVTFSGOYNISWR 120
 80 tshmdvfrhmaddifsvniltldqsgnyfgecgslraesikrappfnvtvtfsgynisrr 139
 QY 121 SDVEDAPFYMLGKLOYELQYRNRCDPWASPRKLTSDRSYSLPLEFRKSSYELO 180
 Db 140 sdyedpafymkgkloyelqyrnrgdpwasprrkltsdsvslplefrkssyeiq 199
 QY 181 VRAGPMGSSSYOGTSEWSMDPVITFOTGSEELKEGMNPH 218
 Db 200 vragpmpgsssyggtsewsmdpvlftgseelkegmnp 237

Search completed: June 28, 2002, 07:46:28
 Job time: 343 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:46:28 ; Search time 110.69 Seconds

(without alignments)
162.562 Million cell updates/sec

Title: US-09-825-561A-10

Perfect score: 850

Sequence: 1 MRSSPCNMERIVICLWVPL.....LLQKMIHQHLSRTHGSEDS 162

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	850	100.0	162	21	AA18623
2	695.5	81.8	519	21	AA18627
3	486	57.2	146	21	AA18624
4	394	46.4	510	21	AA18628
5	212	24.9	40	21	AA18625
6	176	20.7	32	21	AA18626
7	103.5	12.2	133	21	AA18625
8	99.5	11.7	114	16	AA18625
9	99.5	11.7	114	16	AA18625
10	99.5	11.7	114	16	AA18625
11	99.5	11.7	114	17	AA18625

12	99.5	11.7	114	17	AA18625	Generic mammalian
13	99.5	11.7	114	19	AA18625	Simian epithelium
14	99.5	11.7	114	20	AA18625	Simian epithelium
15	99.5	11.7	114	21	AA18625	Mature simian epit
16	99.5	11.7	114	22	AA18625	Simian ERF (SETF)
17	99.5	11.7	162	16	AA18625	Human interleukin-
18	99.5	11.7	162	16	AA18625	Human IL-15. Homo
19	99.5	11.7	162	17	AA18625	Simian epithelium
20	99.5	11.7	162	17	AA18625	Human epithelium-d
21	99.5	11.7	162	17	AA18625	Human interleukin-
22	99.5	11.7	162	18	AA18625	wild-type interlu
23	99.5	11.7	162	18	AA18625	Human interleukin-
24	99.5	11.7	162	19	AA18625	Human interleukin-
25	99.5	11.7	162	19	AA18625	Simian epithelium
26	99.5	11.7	162	20	AA18625	Simian epithelium
27	99.5	11.7	162	21	AA18625	Amino acid sequenc
28	99.5	11.7	162	21	AA18625	Human interleukin-
29	99.5	11.7	162	21	AA18625	Human interleukin-
30	99.5	11.7	162	22	AA18625	Human interleukin-
31	99.5	11.7	162	22	AA18625	Simian ERF (SETF)
32	99.5	11.7	162	22	AA18625	Human interleukin-
33	99.5	11.7	162	22	AA18625	Human IL-15. Homo
34	99.5	11.7	114	16	AA18625	Simian interleukin
35	99.5	11.7	114	17	AA18625	Human mature epith
36	99.5	11.7	114	19	AA18625	Human epithelium d
37	99.5	11.7	114	20	AA18625	Human epithelium-d
38	99.5	11.7	114	21	AA18625	Mature human epith
39	99.5	11.7	114	22	AA18625	Human ERF (hERF) m
40	99.5	11.7	122	17	AA18625	Recombinant flag s
41	99.5	11.7	162	16	AA18625	Simian interleukin
42	99.5	11.7	162	16	AA18625	Simian IL-15. Cer
43	99.5	11.7	162	17	AA18625	Human epithelium d
44	99.5	11.7	162	17	AA18625	Simian epithelium-
45	99.5	11.7	162	17	AA18625	Simian interleukin

ALIGNMENTS

RESULT	1
ID	AA18623 standard; Protein: 162 AA.
AC	AA18623;
XX	XX
DT	22-JAN-2001 (first entry)
DE	XX
XX	XX
KW	zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;
KW	tumorigenesis; leukaemia; hematopoiesis; B cell tumour.
XX	XX
OS	Homo sapiens.
XX	XX
PN	WO200053761-A2.
XX	XX
PD	14-SEP-2000.
XX	XX
PF	09-MAR-2000; 2000MO-US06067.
XX	XX
PR	09-MAR-1999; 99US-0264908.
PR	11-MAR-1999; 99US-0265992.
PR	01-JUL-1999; 99US-0142013.
XX	XX
PA	(ZYMO) ZYMOGENETICS INC.
PI	Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA;
PI	Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX	XX
DR	WPI; 2000-565600/52.
XX	XX
DR	N-PSDB; AA175552.
XX	XX
PT	New human cytokine, designated zalphall ligand, useful for stimulating

[illegible]

PR	11-MAR-1999;	99US-0265992.	
PR	01-JUL-1999;	99US-0142013.	
PA	(ZYMO) ZYMOGENETICS INC.		
XX			
PI	Novak JE, Presneil SR, Sprecher CA, Foster DC, Holly RD, Gross JA,		
PI	Johnston JV, Nelson AJ, Dillon SR, Hammond AK,		
XX			
DR	WPI: 2000-565600/52.		
DR	N-PSDB; AAA75602.		
PT	New human cytokine, designated zalphall ligand, useful for stimulating		
PT	the proliferation and/or development of haematopoietic cells in vitro		
PT	and in vivo, and for treating tumourigenesis -		
XX			
PS	Example 31; Page 239-240; 256pp; English.		
XX			
CC	The present sequence represents a MBP-mouse zalphall ligand fusion in		
CC	the plasmid pTAP126. zalphall ligand is a cytokine. The zalphall ligand		
CC	is useful for stimulating the proliferation and development of		
CC	haematopoietic cells in vitro and in vivo. zalphall ligand		
CC	polynucleotides can be used as primers or probes for cloning the		
CC	zalphall gene. The zalphall ligand is useful for treating tumourigenesis.		
CC	A zalphall ligand-saporin fusion toxin may be used for treating		
CC	leukaemias and lymphomas. Antagonists against zalphall ligand are		
CC	useful as research reagents for characterizing ligand-receptor		
CC	interaction. Antagonists are also useful for inhibiting expansion,		
CC	proliferation, activation and differentiation of cells involved in		
CC	regulating hematopoiesis. The zalphall ligand may also be used to		
CC	stimulate an immune response against B cell tumour, a virus, a parasite		
CC	or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,		
CC	agonists and antibodies are also useful for the detection, diagnosis,		
CC	prevention, and treatment of diseases associated with a zalphall ligand		
CC	genetic defect.		
XX			
SO	Sequence 510 AA;		
Query Match	46.4%; Score 394; DB 21; Length 510;		
Best Local Similarity	62.0%; Pred. No. 2.5e-35;		
Matches	75; Conservative 19; Mismatches 27; Indels 0; Gaps 0;		
OY	33 DEHMTRMROLIDIVDOLKNYVNDLVEPLPADEVETNCWMSAFSCFOKAOLKSANTGNN 92		
DB	330 dTLLIRTLHLDIVGKLYIENDLPellIsapgdvKknccehaafacfgkAkIkpenpnn 449		
OY	93 ERIINWSIKKILKRKRPSPNAGRGROKHLTGPCSDSEYKKRPKEPFLERKRSILQKTHOHL 152		
DB	450 KfIdIdIvqLrrITparrgkKqKhIakpcsdseYekrTpeIlerIkwlIkmIhnl 509		
OY	153 s 153		
DB	510 s 510		
RESULT 5			
AAB18625			
ID	AAB18625 standard; Peptide: 40 AA.		
XX			
XX	AAB18625;		
XX			
DT	22-JAN-2001 (first entry)		
XX			
DE	Antigenic peptide derived from a human zalphall ligand polypeptide.		
XX			
KW	zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;		
KW	tumourigenesis; leukaemia; hematopoiesis; B cell tumour.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200053761-A2.		
XX			
PD	14-SEP-2000.		

```

XX 09-MAR-2000; 2000MO-US06067.
PF 09-MAR-1999; 99US-0264908.
XX 11-MAR-1999; 99US-0265992.
PR 01-JUL-1999; 99US-0142013.
XX (ZYMO ) ZYMOGENETICS INC.
XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA;
PI Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
DR WPI: 2000-565600/52.
XX New human cytokine, designated zalpahal ligand, useful for stimulating
PT the proliferation and/or development of haematopoietic cells in vitro
XX and in vivo, and for treating tumourigenesis -
PS Example 34; Page 227; 256pp; English.
XX The present sequence was used to raise antibodies, and is derived from
CC a human zalpahal ligand polypeptide. Zalpahal ligand is a cytokine.
CC The zalpahal ligand is useful for stimulating the proliferation and
CC development of haematopoietic cells in vitro and in vivo. Zalpahal
CC ligand polynucleotides can be used as primers or probes for cloning the
CC zalpahal gene. The zalpahal ligand is useful for treating tumourigenesis.
CC A zalpahal ligand-saporin fusion toxin may be used for treating
CC leukemias and lymphomas. Antagonists against zalpahal ligand are
CC useful as research reagents for characterizing ligand-receptor
CC interaction. Antagonists are also useful for inhibiting expansion,
CC proliferation, activation and differentiation of cells involved in
CC regulating hematopoiesis. The zalpahal ligand may also be used to
CC stimulate an immune response against B cell tumour, a virus, a parasite
CC or a bacterium. The zalpahal polypeptides, polynucleotides, antagonists,
CC agonists and antibodies are also useful for the detection, diagnosis,
CC prevention, and treatment of diseases associated with a zalpahal ligand
CC genetic defect.
XX Sequence 40 AA:
SQ
Query Match 24.9%; Score 212; DB 21; Length 40;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 32 ODRHMRMQLIDIVDQKKNYNDLVPEFLPAPEDEVENC 71
DB 1 gdrhmrmqlidivdqknynvdlvpeflpapedevenc 40
RESULT 6
AABI8626
ID AABI8626 standard; Peptide: 32 AA.
XX AABI8626;
AC
XX 22-JAN-2001 (first entry)
DT
XX Antigenic peptide derived from a human zalpahal ligand polypeptide.
DE
XX zalpahal ligand; cytokine; haematopoietic cell proliferation; lymphoma;
KW tumourigenesis; leukaemia; hematopoiesis; B cell tumour.
XX Homo sapiens.
OS
XX WO200053761-A2.
PN
XX 14-SEP-2000.
PD
XX 09-MAR-2000; 2000MO-US06067.
PF
XX 09-MAR-1999; 99US-0264908.
PR 11-MAR-1999; 99US-0265992.
XX

```

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PR 01-JUL-1999; 99US-0142013.
XX (ZYMO ) ZYMOGENETICS INC.
XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA;
PI Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
DR WPI: 2000-565600/52.
XX New human cytokine, designated zalpahal ligand, useful for stimulating
PT the proliferation and/or development of haematopoietic cells in vitro
XX and in vivo, and for treating tumourigenesis -
PS Example 34; Page 227; 256pp; English.
XX The present sequence was used to raise antibodies, and is derived from
CC a human zalpahal ligand polypeptide. Zalpahal ligand is a cytokine.
CC The zalpahal ligand is useful for stimulating the proliferation and
CC development of haematopoietic cells in vitro and in vivo. Zalpahal
CC ligand polynucleotides can be used as primers or probes for cloning the
CC zalpahal gene. The zalpahal ligand is useful for treating tumourigenesis.
CC A zalpahal ligand-saporin fusion toxin may be used for treating
CC leukemias and lymphomas. Antagonists against zalpahal ligand are
CC useful as research reagents for characterizing ligand-receptor
CC interaction. Antagonists are also useful for inhibiting expansion,
CC proliferation, activation and differentiation of cells involved in
CC regulating hematopoiesis. The zalpahal ligand may also be used to
CC stimulate an immune response against B cell tumour, a virus, a parasite
CC or a bacterium. The zalpahal polypeptides, polynucleotides, antagonists,
CC agonists and antibodies are also useful for the detection, diagnosis,
CC prevention, and treatment of diseases associated with a zalpahal ligand
CC genetic defect.
XX Sequence 32 AA:
SQ
Query Match 20.7%; Score 176; DB 21; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e-12;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 122 CPSCDSYEKKRPKEFLERFKSLQKMHQHL 153
DB 1 cpscdsyekkpkpkeflerfkslqkxmhqhl 32
RESULT 7
AA54825
ID AA54825 standard; Protein: 135 AA.
XX AA54825;
AC
XX 04-FEB-2000 (first entry)
DT
XX Human Interleukin-15 protein sequence.
DE
XX Interleukin-15; IL-15; antisense inhibitor; untranslated region; 5'UTR;
KW 3'UTR; human; infection; inflammation; tumour; therapy; diagnosis.
XX Homo sapiens.
OS
XX US5985663-A.
PN
XX 16-NOV-1999.
PD
XX 25-NOV-1998; 98US-0200141.
PF
XX 25-NOV-1998; 98US-0200141.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Bennett CF, Cowser LM;
PI
XX WPI: 2000-022283/02.
DR

```

DR N-PSDB; AAR37358.
 XX Antisense compound useful for inhibiting human interleukin-15
 PT expression useful for treating diseases associated with interleukin-15
 PT expression -
 XX
 PS Example 13: Column 43-44: 31pp; English.
 XX
 CC This sequence is the human interleukin-15. The invention relates to
 CC antisense compounds that are targeted to a 5' or 3' untranslated region
 CC (5'UTR or 3'UTR) of a nucleic acid molecule encoding human interleukin-15
 CC (IL-15), and inhibit the expression of human IL-15. The antisense
 CC inhibitors are useful for inhibiting expression of IL-15 in human
 CC cells or tissues in vitro, for treating humans or other animals suspected
 CC of having or being prone to a disease associated with IL-15 expression,
 CC e.g. infections, inflammation or tumours. The inhibitors can also be used
 CC for research or diagnostic purposes. Using antisense compounds
 CC specifically and effectively inhibits IL-15 function.

Sequence 135 AA:

Query Match 12.2%; Score 103.5; DB 21; Length 135;
 Best Local Similarity 26.7%; Pred. No. 0.0014;
 Matches 31; Conservative 22; Mismatches 48; Indels 15; Gaps 5;

OY 43 IDIVDQKKNVNDLPEF-----LPAPDYETNCMSATSCF---QKAKLSANTGNNE 93
 DB 24 vnvvsdtkk-iedlqgmhdatlytesdvpsckvtamkcfllqlqvistsgdsahnd 82
 OY 94 RIINVSIRKIKRKRPSTNAGROKHRLTGPCDSYEKKPKPELEPKSLDKMHI 149
 DB 83 tvenllil--lamslssngvtes---gkceceeleekniketlqsfvnlvqmfin 133

RESULT 8

AAR83310
 ID AAR83310 standard; Protein; 114 AA.

AC AAR83310;

DT 02-FEB-1996 (first entry)

XX Human interleukin-15 mature polypeptide.

DE Interleukin-15; epithelium-derived T-cell factor; T lymphocyte.

XX Homo sapiens.

XX W09527722-A.

XX 19-OCT-1995.

XX 06-APR-1994; 94WO-US03793.

XX 06-APR-1994; 94WO-US03793.

XX (IMMV) IMMUNEX CORP.

XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;

XX PI Rauch C.

XX WPI; 1995-373556/48.

XX N-PSDB; AAT00527.

XX Isolated DNA encoding polypeptide with mammalian IL-15 activity - which

XX PT stimulates proliferation and differentiation of T cells, used for

XX PT treating carcinoma(s), melanomas, etc. and viral infections

XX PS Claim 23: Page 30; 48pp; English.

XX A simian species of IL-15 (sIL-15) was purified and its AA

XX CC sequence and cDNA sequence analysed (see AAR83309, AAR83436,

CC AAT00524, AAT00525). Both the simian and the human ORFs encode
 CC a precursor polypeptide (AAR83436, AAR83438). The precursor
 CC polypeptides each comprise a 48-AA leader sequence and a sequence
 CC encoding mature simian or human IL-15 polypeptides. The active
 CC simian and human IL-15 polypeptides are disclosed in AAR83309 &
 CC AAR83310 respectively. The invention also comprises other mammalian
 CC IL-15, including human IL-15, that hybridise to probes defined by
 CC AAR83438. A plasmid contg. a recombinant clone of human IL-15
 CC cDNA was deposited with ATCC on Feb. 19 1993 under ATCC 69245.
 CC The deposit was named 141-HETF. AAR83435 is a mammalian mature
 CC IL-15 polypeptide. It is a generic sequence which encompasses both
 CC AAR83309 (simian) and AAR83310 (human) IL-15 mature polypeptides.

XX Sequence 114 AA;

Query Match 11.7%; Score 99.5; DB 16; Length 114;
 Best Local Similarity 25.9%; Pred. No. 0.0031;
 Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;

OY 43 IDIVDQKKNVNDLPEF-----LPAPDYETNCMSATSCF---QKAKLSANTGNNE 93
 DB 3 vnvvsdtkk-iedlqgmhdatlytesdvpsckvtamkcfllqlqvistsgdsahnd 61
 OY 94 RIINVSIRKIKRKRPSTNAGROKHRLTGPCDSYEKKPKPELEPKSLDKMHI 149
 DB 62 tvenllil--lamslssngvtes---gkceceeleekniketlqsfvnlvqmfin 112

RESULT 9

AAR83435
 ID AAR83435 standard; Protein; 114 AA.

AC AAR83435;

DT 02-FEB-1996 (first entry)

XX Mammalian interleukin-15 mature polypeptide.

DE Interleukin-15; epithelium-derived T-cell factor; T lymphocyte.

XX Mammalian.

XX Key Location/Qualifiers

XX MISC-difference 52 /label= L,H

XX MISC-difference 57 /label= A,T

XX MISC-difference 58 /label= S,D

XX MISC-difference 73 /label= S,I

XX MISC-difference 80 /label= V,I

XX W09527722-A.

XX 19-OCT-1995.

XX 06-APR-1994; 94WO-US03793.

XX 06-APR-1994; 94WO-US03793.

XX (IMMV) IMMUNEX CORP.

XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;

XX PI Rauch C.

XX WPI; 1995-373556/48.

XX Isolated DNA encoding polypeptide with mammalian IL-15 activity - which

XX PT stimulates proliferation and differentiation of T cells, used for

XX PT treating carcinoma(s), melanomas, etc. and viral infections

CC This sequence represents mature simian epithelium-derived T-cell factor
 CC (ETF). This is a previously unidentified T-cell growth factor which
 CC stimulates precursor or mature CD4+ and CD8+ T-lymphocytes to proliferate
 CC and differentiate. It also promotes proliferation of the gastrointestinal
 CC epithelium. The protein can be used to promote long-term in vitro culture
 CC of T-lymphocytes and T-cell lines. ETF can be used for treating HIV
 CC infection, HIV-associated diseases, and other diseases or conditions
 CC where stimulation of T-cell proliferation would be desirable e.g., it
 CC could be used to augment the destruction of tumour cells or virally-
 CC infected cells. ETF may also be used to treat or prevent gastrointestinal
 CC disease, including chemotherapy and radiotherapy associated enteritis,
 CC gastroenteritis, colitis, inflammatory bowel disease and villus atrophic
 CC disorders. Chemotherapy and radiotherapy associated enteritis (gut
 CC toxicity) results in bleeding and sepsis due to gastrointestinal flora
 CC entering the blood, and thus can limit the dosage of therapeutic agent
 CC administered to a cancer patient. ETF may therefore be used to increase
 CC the tolerated doses radiotherapy and chemotherapy.

XX Sequence 114 AA;

Query Match 11.7%; Score 99.5; DB 21; Length 114;
 Best Local Similarity 25.9%; Pred. No. 0.0031;
 Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;

QY 43 IDIVDOKNVNDLVPF-----LPAPDYVFNCEWAFSCF---QKQKSAWNGNE 93
 Db 3 vnvvsdlkx-iedlqgmhdatlyesdvhpckvltamkcfllqlqvistlesgdasind 61
 QY 94 RIINVSIRKLRRKPPSTNAGRQKRLCTPCSDSYEKRPPEFLERFKSLQKMH 149
 Db 62 tvenlll--lannslnsgnvtes---gckeceeleeknikelfgfvhivqmfan 112

Search completed: June 28, 2002, 07:46:29
 Job time: 344 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:44:32 ; Search time 63.41 Seconds
(without alignments)
441.968 Million cell updates/sec

Title: US-09-825-561A-10

Perfect score: 850

Sequence: 1 MRSSPGNMERIVICLAWIFL.....LLQKMHQHLSSRTGSEDS 162

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	850	100.0	162	4	Q9HBE4	Q9HBE4 homo sapien
2	486	57.2	146	11	Q9ES17	Q9ES17 mus musculu
3	91.5	10.8	367	11	Q05208	Q05208 mus musculu
4	83.5	9.8	3052	12	Q82933	Q82933 johnsongras
5	83	9.8	899	2	Q9R2J7	Q9R2J7 shigella so
6	83	9.8	899	2	Q52336	Q52336 salmonella
7	81.5	9.6	566	5	Q9VVE8	Q9VVE8 drosophila
8	81	9.5	163	5	Q966R0	Q966R0 dictyostell
9	81	9.5	383	5	Q9VUI7	Q9VUI7 drosophila
10	81	9.5	414	5	Q9NK60	Q9NK60 drosophila
11	79.5	9.4	187	13	Q9W756	Q9W756 gallus gall
12	79.5	9.4	1006	11	Q9JY09	Q9JY09 mus musculu
13	78	9.2	305	11	Q9JY48	Q9JY48 mus musculu
14	77	9.1	319	4	Q96LJ4	Q96LJ4 homo sapien
15	76.5	9.0	421	5	Q9VY89	Q9VY89 drosophila
16	76.5	9.0	424	5	Q23239	Q23239 calliphora

17	75.5	8.9	187	13	Q9DEV5	Q9DEV5 gallus gall
18	75.5	8.9	216	6	Q9BER3	Q9BER3 didelphis m
19	75.5	8.9	336	11	Q62612	Q62612 ratius norv
20	75.5	8.9	406	5	Q22975	Q22975 caenorhabdi
21	75.5	8.9	566	11	Q62611	Q62611 ratius norv
22	75	8.8	357	4	Q96C15	Q96C15 homo sapien
23	74.5	8.8	286	16	Q9CPY5	Q9CPY5 ureaplasma
24	74.5	8.8	441	10	Q9C5F0	Q9C5F0 arabidopsis
25	74.5	8.8	484	6	Q9MZ13	Q9MZ13 bos taurus
26	74.5	8.8	848	4	Q75141	Q75141 homo sapien
27	74.5	8.8	1066	10	Q9AV01	Q9AV01 oryza sativ
28	74	8.7	143	13	Q9IAC7	Q9IAC7 meleagris g
29	74	8.7	201	4	Q9H6V1	Q9H6V1 homo sapien
30	74	8.7	440	10	Q9M2E9	Q9M2E9 arabidopsis
31	74	8.7	457	11	Q9CXY7	Q9CXY7 mus musculu
32	74	8.7	599	12	Q71211	Q71211 grapevine 1
33	74	8.7	599	12	Q39854	Q39854 grapevine 1
34	74	8.7	953	11	Q60442	Q60442 ricecelus
35	74	8.7	2197	5	Q96296	Q96296 plasmodium
36	73.5	8.6	396	5	Q967E2	Q967E2 chironomus
37	73.5	8.6	545	5	Q9W3H8	Q9W3H8 drosophila
38	73.5	8.6	565	16	Q9V099	Q9V099 staphylococ
39	73.5	8.6	629	8	Q9T708	Q9T708 ginkgo bilo
40	73.5	8.6	770	5	Q44014	Q44014 leishmania
41	73.5	8.6	868	5	Q9NAB8	Q9NAB8 caenorhabdi
42	73.5	8.6	2118	5	Q76904	Q76904 drosophila
43	73.5	8.6	2328	5	Q9WMA7	Q9WMA7 drosophila
44	73.5	8.6	2531	5	Q9CPH4	Q9CPH4 drosophila
45	73	8.6	556	5	Q18181	Q18181 caenorhabdi

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	162 AA.
Q9HBE4	Q9HBE4			
AC	Q9HBE4			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	INTERLEUKIN 21.			
GN	IL21.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20531754; PubMed=11081504;			
RX	Parish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C.,			
RA	Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S.,			
RA	Burkhead S., Heipel M., Brandt C., Kullper J.L., Kramer J.,			
RA	Conklin D., Presnell S.R., Berry J., Shiohara F., Bort S., Hamby K.,			
RA	Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T.,			
RA	Rayond F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,			
RA	Maurer M., Kauschansky K., Holly R.D., Foster D.;			
RT	"Interleukin 21 and its receptor are involved in NK cell expansion and			
RT	regulation of lymphocyte function.";			
RL	Nature 408:57-63(2000).			
DR	EMBL; AF254069; AAG29348.1; -			
SO	SEQUENCE 162 AA; 18652 MW; 54EPD4EED3AB97FE CRC64;			

Query Match 100.0%; Score 850; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.1e-79;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRSSPGNMERIVICLAWIFGLVHKSSSGODRHRIMRQLDIYDQKNTVNDLVEEF 60
DB	1	MRSSPGNMERIVICLAWIFGLVHKSSSGODRHRIMRQLDIYDQKNTVNDLVEEF 60
QY	61	LPAPDEVTCNCEWASCFQKALKSANTGNMERITINVSIIKKKKRPSTNAGRRQKRL 120

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Db 61 LPAPEDVETNCWMSAFSCFOKALQKSAANTGNERNRINVSIIKKLRKRPSTNAGRQKHRL 120
QY 121 TCPSCDSEYKKPKPEFLERKSLLOKMIHOHLSRRHGSDDS 162
Db 121 TCPSCDSEYKKPKPEFLERKSLLOKMIHOHLSRRHGSDDS 162

RESULT 2
Q9ES17 PRELIMINARY; PRT; 146 AA.
AC 09ES17;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INTERLEUKIN 21.
GN IL21.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20531754; PubMed=11081504;
RA Parish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C.,
RA Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S.,
RA Burkhead S., Heipel M., Brandt C., Kuiper J.L., Kramer J.,
RA Conklin D., Presnell S.R., Berry J., Shiota F., Bort S., Hamby K.,
RA Raynd S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T.,
RA Maurand F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,
RA Maurer M., Kauschansky K., Holly R.D., Foster D.;
RT "interleukin 21 and its receptor are involved in NK cell expansion and
RT regulation of lymphocyte function.";
RL Nature 408:57-63(2000).
DR EMBL: AF254070; ANG29349.1; -.
DR MGD: MGT:1890474; IL21
SQ SEQUENCE 146 AA; 16811 MW; D2527ED95BA15194 CRC64;

Query Match 57.2%; Score 486; DB 11; Length 146;
Best Local Similarity 63.0%; Pred. No. 2,6e-42;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MEIVICLVAVIFGLVHKSSSGODRHMRQIDIVDQKKNVNDLVPELPAPEDV 67
|||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MERTVLCVAVIFGLVHNSSPQGPRLRLRLHLDIYEOLKIYENDLPILLSAPQV 60
|||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 68 ETNCWMSAFSCFOKALQKSAANTGNERNRINVSIIKKLRKRPSTNAGRQKHRLTSCDS 127
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 KGAECENAAFCQKAKLFSNPENNTFTIIDVAQLRRRLPARGGKKOKHIAKCPSCDS 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 128 YEKRPKEFLERKSLLOKMIHOHLS 153
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 YEKRPKEFLERKSLLOKMIHOHLS 146
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
ID 005208 PRELIMINARY; PRT; 567 AA.
AC 005208;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE STZL PROTEIN PRECURSOR.
GN IL1RL1 OR STZL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RX MEDLINE=93170492; PubMed=7916701;

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RA Yanagisawa K., Takagi T., Tsukamoto T., Tetsuka T., Tomimaga S.;
RT "Presence of a novel primary response gene STZL, encoding a product
RT highly similar to the interleukin 1 receptor type 1.";
RL FEBS Lett. 318:83-87(1993).
DR EMBL: D13695; BAA02854.1; -.
DR MGD: MGT:98427; IL1RL1.
DR InterPro: IPR003598; IG_C2.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR004075; Intriknl_receptorI.
DR InterPro: IPR002052; N6_Mtase.
DR InterPro: IPR00157; TIR.
DR Pfam: PF00047; IG_3.
DR Pfam: PF01582; TIR; 1.
DR PRINTS: PRO1537; INTRILN1RLF.
DR SMART: SM00408; IGC2; 2.
DR SMART: SM00255; TIR; 1.
DR PROSITE: PS00092; N6_MTASE; UNKNOWN_1.
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 567 STZL PROTEIN.
SQ SEQUENCE 567 AA; 64801 MW; 9228CE227D95B0BC CRC64;

Query Match 10.8%; Score 91.5; DB 11; Length 567;
Best Local Similarity 25.6%; Pred. No. 0.45;
Matches 33; Conservative 20; Mismatches 39; Indels 37; Gaps 7;

QY 47 DOLKNVNDVPEEPFAPEDVETNCWMSAFSCFOKALQKSAANTGNERNRINVSIIKKLRK 106
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 76 DLK-----FLPARE-----DSGITACV-----IRSNL-NKGYLWVTHK---K 113
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 107 PSTN-----AGRRQKHRLTSCDSYKKPKPEFLERKSLLOKMIHOH----- 151
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 114 PSCNIPYLYWSTVSGDKNFKIKCPITIDLYNMTAPYQWFKCKALQEPFRFRAHRSYLF 173
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 152 LSSRTGSE 160
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 174 IDNVTHDE 182
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
ID 082933 PRELIMINARY; PRT; 3052 AA.
AC 082933;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE VIRAL PROTEINS.
OS Johnsongrass mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=31742;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94200956; PubMed=8150599;
RA Gough K.H., Shukla D.D.;
RT "the nucleotide sequence of Johnson grass mosaic potyvirus genomic
RT RNA.";
RL Intervirology 36:181-192(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Gough K.H.;
RN Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Nurbayati E.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z26920; CAAB1549.1; -.
DR MEROPS: C04.011; -.
DR MEROPS: C06.001; -.
DR MEROPS: S30.001; -.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase_C.

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DR InterPro: IPR001730; Peptidase_C4.
DR InterPro: IPR001436; Peptidase_C6.
DR InterPro: IPR001592; Poly_coat.
DR InterPro: IPR002540; Poly_P1.
DR InterPro: IPR001205; RNA_pol_P3D.
DR Pfam: PF002270; DEAD_1.
DR Pfam: PF00863; Peptidase_C4_1.
DR Pfam: PF00851; Peptidase_C6_1.
DR Pfam: PF00767; Poly_coat_1.
DR Pfam: PF01577; Poly_P1_1.
DR Pfam: PF00680; RNA_dep_RNA_pol_1.
DR PRINTS: PR00966; NTPOTPTASE.
DR SMART: SM00487; DEXDC_1.
DR SMART: SM00490; HELICC_1.
KM ATP-binding: Helicase.
FT CHAIN 239 699 HELPER COMPONENT (HC).
FT CHAIN 700 1046 PROTEASE3.
FT CHAIN 1047 1098 6K1.
FT CHAIN 1099 1757 CYTOPLASMIC INCLUSION (CI).
FT CHAIN 1758 1803 6K2.
FT CHAIN 1804 1991 SMALL NUCLEAR INCLUSION/VIRUS ATTACHED
FT CHAIN 1992 2233 PROTEIN.
FT CHAIN 2234 2749 SMALL NUCLEAR INCLUSION/PROTEASE.
FT CHAIN 2750 3052 LARGE NUCLEAR INCLUSION/POLYMERASE.
FT CHAIN 3052 347247 COAT PROTEIN.
SQ SEQUENCE 3052 AA; 347247 MW; 08CD8831A73EBCA9 CRC64;

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Query Match 9.8%; Score 83.5; DB 12; Length 3052;
Best Local Similarity 23.1%; Pred. No. 21;
Matches 25; Conservative 23; Mismatches 57; Indels 3; Gaps 3;

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OY 45 IYDOLKYNVNDLVPEFLPAPEDVETNCWMSAFSCFOKAQKSNKNGNRIINVSIIKLK 104
DB 220 LVNALDOYEED-VKQICHSFDEARAFWKGFTENHTPAQRREHDTNHPV-MSVEECG 277
OY 105 RKPESTNAGRQKHRLTQPCSC-DSEYKPKPEFLERFKSLQKMIHQH 151
DB 278 RRAAMLENAFHQGFRTCKHCFQTFDEHSDSEVCERIHNAIDRIEQRN 325

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RESULT 5
OYR2J7 PRELIMINARY; PRT; 899 AA.
AC OYR2J7;
RT 01-MAY-2000 (Tremblrel. 13, Created)
RT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
RT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RELAXASE.
GN NIKB.
OS Shigella sonnei.
OC Plasmid Colid-P9.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Shigella.
OX NCBI_TaxID=624;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P9;
RA Sampei G., Mizobuchi K.;
RT "Organization and diversification of plasmid genomes: complete
RT nucleotide sequence of the Colid-P9 genome."
RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB021078; BAA75140.1; -.
KW Plasmid.
SO SEQUENCE 899 AA; 103977 MW; E7DB0164C54914E3 CRC64;

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Query Match 9.8%; Score 83; DB 2; Length 899;
Best Local Similarity 22.5%; Pred. No. 5.8;
Matches 34; Conservative 22; Mismatches 55; Indels 40; Gaps 7;
OY 27 SSSGQODRHMI RMQLIDYDOLKYNVNDLVPEFLPAPEDVETNCWMSAF---SCFOKAQ 83

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DB 38 SSSQAEQPHRSFSLVYATRLN-----ESTVALVDMKGCWVNFYVTCFHNCT 91
OY 84 LKSANTGNERRIINVSIIKLKRPSTNAGROKHL--TCP-----SCSYEKRPK 134
DB 92 SLETAADMEYI-----ARQAHYKDDTDFVFHYIILWSHESPRPE 133
OY 135 EFLERFKSLQK---IHQHLSSRTGSEDS 162
DB 134 QYIDSVRHTKSLGLADHQVYA-VHDTDN 163

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RESULT 6
OY2336 PRELIMINARY; PRT; 899 AA.
ID OY2336;
AC OY2336;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE NIKB.
GN NIKB.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE OF 895-899 FROM N.A.
RC STRAIN=DRD-11;
RX MEDLINE=96198148; PubMed=8626273;
RA Furuya N., Komano T.;
RT "Nucleotide sequence and characterization of the trbABC region of the
RT IncII plasmid R64: existence of the pnd gene for plasmid maintenance
RT within the transfer region."
RT J. Bacteriol. 178:1491-1497(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DRD-11;
RX MEDLINE=91177811; PubMed=1848841;
RA Furuya N., Nisiooka T., Komano T.;
RT "Nucleotide sequence and functions of the orf1 operon in IncII plasmid
RT R64."
RT J. Bacteriol. 173:2231-2237(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=DRD-11;
RX MEDLINE=92011438; PubMed=1917882;
RA Furuya N., Komano T.;
RT "Determination of the nick site at orf1 of IncII plasmid R64: global
RT similarity of orf1 structures of IncII and IncP plasmids."
RT J. Bacteriol. 173:6612-6617(1991).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=DRD-11;
RX MEDLINE=98053841; PubMed=9393692;
RA Furuya N., Komano T.;
RT "Mutational analysis of the R64 orf1 region: requirement for precise
RT location of the Nika-binding sequence."
RT J. Bacteriol. 179:7291-7297(1997).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=DRD-11;
RX MEDLINE=98268996; PubMed=9603870;
RA Yoshida T., Furuya N., Ishikura M., Isobe T., Haino-Fukushima K.,
RA Ogawa T., Komano T.;
RT "Purification and characterization of thin pili of IncII plasmids

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[illegible]

RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunbok B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferriz C., Ferreira S., Flitschmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glöck A., Gong F., Gorrell J.T., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heilmann T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ilegaram C.,
RA Udall M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Mosherl A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskens D.R., Paclab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassenaar D.A., Weinstein G.M., Weissendach J.,
RA Williams S.M., Woodgate T., Wooley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveril J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
DB EMBL: AE003492; AAF48250.1; -
DB FlyBase: FBgn0030469; CC15745;
QO SQUENCE 566 AA; 60620 MW; 31F4M1FAAE427F CRC64;

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Query Match          9.6%; Score 81.5; DB 5; Length 566;
Best Local Similarity    26.1%; Pred. No. 4.8;
Matches      24; Conservative   21; Mismatches   40; Indels    7; Gaps     3;

QY      66 DVFENCMSAFS--CQKQLKSANTGNNERNINYSIKKLKRKPSTNNAQRKHRLTOP 123
           || :|||::| :|||||::|| |
DB      120 DIGPFCVWSISLALRKLAKRKAPFFGVQV---GLARDSEISSITRTTNTYNASNP 175
           || :|||::| :|||||::|| |

QY      124 SCDSYEKKKPKPEFLERFKSL-OKMIHOLLS 154
           || :|||::| :|||||::|| |
DB      176 SKTEREGKPYOQLIDOFQAMIVQOOOQOOLSN 207
           || :|||::| :|||||::|| |

RESULT      8
0966R0      PRELIMINARY; PRT; 163 AA.
AC      0966R0:
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE      CALCIUM BINDING PROTEIN CBP9.
GN      CBP1.
OS      Dictyostelium discoideum (slime mold).
OC      Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
NCBI_TaxID=44689;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-KAX4.
RA      Mishio K., Yokoyama M., Maeda M.;
RT      "Novel calcium binding proteins in Dictyostelium.";
RL      Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
EMBL: AB070450; BAB63908.1; -.
CC      SEQUENCE 163 AA; 18924 MW; AF0BCB3C7FECBEF CRC64;

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Query Match      9.5%  Score 81;  DB 5;  Length 163;
Best Local Similarity 25.5%  Pred. No. 1.3;
Matches 26;  Conservative 17;  Mismatches 51;  Indels 8;  Gaps 2.
OY 53 VNDLVEPEFLAPADVETNCENMFAFSCFOQAQKLSANTNNRRILNIWSIKTKKKRPPSTNA 112
Db 9 LNEKKPILKCDNNKRO-----YSDLDEVLYLTKKNSNPNRPLVLLFKSLNKKLDESDIC 63

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OY 113 GR0KHRLTGPCSDSYEKKP---KEFLERFKSLQKMIHOH 151
 Db 64 FNDIDREISKNCCKRQKPEIDIESFLRFDKNDKMISSH 105

RESULT 9
 ID 09VJL7 PRELIMINARY: PRT: 385 AA.
 AC 09VJL7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE BG:DS02740.8 PROTEIN.
 GN BG:DS02740.8 OR CG17328.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 NC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_Taxid=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RA MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Adganyi A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson R.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Flogel A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Gload C., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Li Z., Liang Y., Lin X.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Ralnet K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Stryckas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissensehl J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003650; AAF3516.1; -.
 DR HSSP: P08046; IALI.
 DR FlyBase: FBgn0028895; BG:DS02740.8.
 DR InterPro: IPR000822; Znf-C2H2.
 DR Pfam: PF00096; znf-C2H2; 6.
 DR SMART: SM00355; ZNF_C2H2; 6.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 6.
 DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 6.
 KW DNA-binding; Metal-binding; Zinc-finger.
 SO SEQUENCE 385 AA; 43943 MW; 24D0EA4C5FD5DA6 CRC64;

Query Match 9.5%; Score 81; DB 5; Length 385;
 Best Local Similarity 22.2%; Pred. No. 3.5;
 Matches 37; Conservative 22; Mismatches 44; Indels 64; Gaps 9;
 OY 12 VTCIAVIF-IGTIVH-KSSSGODRHHIRMROLDIDYDQKNTVNDLVEFLPAPDVF 69
 Db 24 VICNCCITRLGVAFHFKEKCEKNSD---LRLKQYIGLIESNR-----QDAAT 66
 OY 70 NCEWSAFSCFOKAQLKSANTGNERNRINVSIRKLKRKRPSTNAGRQKHRLTGPCSDSYE 129
 Db 67 NMD-----FVEKRLPLPRDSDEEPEYDAKYSK-----RRSR-----YQ 99
 OY 130 KRPKEFLERFKSLQKMIH-----OHLSSRTGSE 160
 Db 100 RRPPEHKKRGRKPRVPMHPCYCHKSKFCIAQLTQHI--RRTGSE 144

RESULT 10
 ID 09NK60 PRELIMINARY: PRT: 414 AA.
 AC 09NK60;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BG:DS02740.8 PROTEIN.
 GN BG:DS02740.8 OR CG17328.
 OS Drosophila melanogaster (Fruit fly)
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 NC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_Taxid=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Y, CN BW SP;
 RA MEDLINE=99403001; PubMed=10471707;
 RA Ashburner M., Mitra S., Roote J., Lewis S.E., Blazer R., Davis T.,
 RA Doyle C., Galle R., George R.A., Harris N., Hartzell G., Harvey D.,
 RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
 RA Palazolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
 RA Celniker S., Rubin G.M.;
 RT "An exploration of the sequence of a 2.9-kb region of the genome of
 RT Drosophila melanogaster: the Adh region.";
 RL Genetics 153:179-219(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Y, CN BW SP;
 RA Celniker S.E., Adganyi A., Arcaina T.T., Baxter E., Blazer R.G.,
 RA Buttenhof C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
 RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
 RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
 RA Lewis S., Li P., Lomolan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
 RA Nixon K., Pacle J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
 RA Sethi H., Sait E., Stryckas R.R., Wan K.H., Weinburg T., Zhang R.,
 RA Zieran L.L., Rubin G.M.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003415; AAF44996.1; -.
 DR HSSP: P08046; IALI.
 DR FlyBase: FBgn0028895; BG:DS02740.8.
 DR InterPro: IPR000345; CYC_C_heme_bind.
 DR InterPro: IPR000822; Znf-C2H2.
 DR Pfam: PF00096; znf-C2H2; 6.
 DR SMART: SM00355; ZNF_C2H2; 6.
 DR PROSITE: PS00028; CYTOCHROME_C; UNKNOWN.1.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 6.
 DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 6.
 KW DNA-binding; Metal-binding; Zinc-finger.
 SO SEQUENCE 414 AA; 47307 MW; 182657C92E2E2D1F CRC64;

Query Match 9.5%; Score 81; DB 5; Length 414;
 Best Local Similarity 22.2%; Pred. No. 3.8;
 Matches 37; Conservative 22; Mismatches 44; Indels 64; Gaps 9;

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QY 12 VICLWVIF-LGTLVH-KSSSGODRHMRMOLIDIVDLKYNVDLVEFLPAPDEVET 69
DB 53 VICNNCTYRLGVAHFHKQCEKNSD--LRKRYLGLILESMR-----QDAPAT 95
QY 70 NCEWSAFSCFOKAOLKSANTGNERNIIVNSIKLKRKPPSTNAGRQKHRLTCSGDSYE 129
DB 96 NTF-----FVEKPLLPQDSDSEEPVDKYSK-----RRSR-----YQ 128
QY 130 KKPKPEFLERFKSLQKMH-----OHLSSRTGSE 160
DB 129 RKPEDEHKKKRKRPVKMPHTCYECHKSKFCAIQLTQHL--RTHTGGE 173

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RESULT 11
Q9W756 PRELIMINARY; PRT; 187 AA.
AC 09W756;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
INTERLEUKIN-15 PRECURSOR (INTERLEUKIN 15 PRECURSOR).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCWL; TISSUE=LIVER;
RA Burnside J., Sofer L.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SC; TISSUE=LIVER;
RA Choi K.D., Lillehoj H.S., Burnside J.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF152927; AAD38392.1; -.
DR EMBL: AF139097; AAF61446.1; -.
DR InterPro: IPR003443; Interleukin_15.
DR Pfam: PF02372; IL15; 1.
SQ SEQUENCE 187 AA; 21964 MW; 470601EBF8837095 CRC64;

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Query Match 9.4%; Score 79.5; DB 13; Length 187;
Best Local Similarity 22.2%; Pred. No. 2.1;
Matches 34; Conservative 19; Mismatches 55; Indels 45; Gaps 6;
15 LAMVIFGLTVHKSSSG-----QDRHMRMOLIDIVDLKYNVDLVEFLPAPDEV 67
DB 52 LTFEFLCAVYPKTEAHNCKMSDVLKDLKTSEDVSLYTN-----TYEDI 100
QY 68 ETNCEWSAFSCF---OKAOLKSANTGNERNIIVNSIKLKRKPPSTNAGRQKHRLT--- 121
DB 101 E--CQEPVNMCFLEMKVILHECD-----IKKSRKHADVNRIMKGNMAREFATYQ 147
QY 122 -----CPSCDSEYKKPKPEFLERFKSLQK 146
DB 148 LNSTAKKCKECEVEEKNFTETIOSFVAVIOR 180

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RESULT 12
Q91Y09 PRELIMINARY; PRT; 1006 AA.
AC 091Y09;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PROTOCADHERIN ALPHA C2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RX MEDLINE-99308636; PubMed-10380929;
RA Wu Q., Maniatis T.;
RT "A striking organization of a large family of human neural cadherin-
RL like cell adhesion genes."
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RX MEDLINE-20202599; PubMed-10716726;
RA Wu Q., Maniatis T.;
RT "Large exons encoding multiple ectodomains are a characteristic
RL feature of protocadherin genes."
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RX MEDLINE-21154914; PubMed-11230163;
RA Wu Q., Zhang T., Cheng J.-F., Kim Y., Grimwood J., Schmutz J.,
RA Dickson M., Noonan J.P., Zhang M.Q., Myers R.M., Maniatis T.;
RT "Comparative dna sequence analysis of mouse and human protocadherin
RL gene clusters."
DR Genome Res. 11:389-404(2001).
DR EMBL: AY013769; AAK26058.1; -.
SQ SEQUENCE 1006 AA; 109491 MW; EB7E29DCA70BC1E CRC64;

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Query Match 9.4%; Score 79.5; DB 11; Length 1006;
Best Local Similarity 29.7%; Pred. No. 15;
Matches 27; Conservative 14; Mismatches 23; Indels 27; Gaps 5;
QY 21 GTLVHKSS-----QGDHMRM-----ROLIDIVDLKYNVDLVE-----FLPAP 64
DB 320 GTLDYESSYQIYVATRGVPVAGKCKVLVDID-----VNDNADEVYLTDLISVP 374
QY 65 EDVETNCEWSAFSCFOKAOLKSANTGNERNI 95
DB 375 EDVALNTVVALIS-----VNDQSGSNRKV 399

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RESULT 13
Q9JY48 PRELIMINARY; PRT; 305 AA.
AC 09JY48;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE ZINC FINGER PROTEIN FLIZ1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=LIVER;
RX MEDLINE-2118925; PubMed-11318609;
RA Dahm K., Nielsen P.J., Muller A.M.;
RT "Transcripts of Fliz1, a nuclear zinc finger protein, are expressed in
RL discrete foci of the murine fetal liver."
DR Genomics 73:194-202(2001).
DR EMBL: AF061961; AAF74513.1; -.
DR MGD; MGI:1930128; Fliz1.
DR InterPro: IPR000571; Zf-CCH.
DR Pfam; PF00642; zf-CCH; 3.
DR SMART; SM00356; ZNF_C3H1; 3.
SQ SEQUENCE 305 AA; 34922 MW; 2F45A0758D56245C CRC64;

```

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Query Match 9.2%; Score 78; DB 11; Length 305;

```


Best Local Similarity 26.2%; Pred. No. 5.4;
Matches 37; Conservative 19; Mismatches 51; Indels 34; Gaps 7;

QY 26 KSSSOG-QDRIMIRMLDIYVOLKNYVNDLPFLPAPDEVENCSAFSCQKQOL 84
DB 88 ETCGSGSDNFKELQOYI---QAEEMAAQPSLLPEEPVKAGAGCTOATAOKN-- 141
QY 85 KSANTGNMERIINVSIKLTKRPPST-----NAGRQKHRLTGPCDSYEKKPPK 134
DB 142 KSKAGHKK---VKQKKMRKWPQGGDKGSRALLKNSSGRQ-----TDEPEKQPR 190
QY 135 EFLERFKSLQKMHQHLSSR 155
DB 191 -----VMSGQFTHQHTVER 205

RESULT 14
096LL4
ID 096LL4 PRELIMINARY; PRT: 319 AA.

01-DEC-2001 (TReMBLrel. 19, Created)
01-DEC-2001 (TReMBLrel. 19, Last sequence update)
01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE CDNA FLJ25402 FIS, CLONE TST02870.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCCL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hoshita T., Hirooka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Motomura M., Kawamura M.,
RA Katakami B., Nagai K., Isogai T., Sato H., Nishikawa T., Sugiyama A.,
RT "NEDO human cDNA sequencing project."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK058131; BAB71677.1;
SQ SEQUENCE 319 AA; 36867 MW; 682FBAE7C6CC936 CRC64;

Query Match 9.1%; Score 77; DB 4; Length 319;
Best Local Similarity 30.6%; Pred. No. 7.2;
Matches 30; Conservative 11; Mismatches 35; Indels 22; Gaps 5;

DB 66 DVETNCMSAFSCFOKAOLKSANTGNMERIINVSIKLTKRPPSTNAGRQKHRLTGPCSC 125
DB 155 DVAS-ERDAFSC-----TVPDELNRIYFRNM-RTPKQDAAKKHISYQCPYC 202
QY 126 D-----SYEKKPREFLERFKSLQKMHQHLSSR 155
DB 203 NRKRAELATSAFLQKKTLLSEF--LLOERIDEHLHTK 238

RESULT 15
09VY89
ID 09VY89 PRELIMINARY; PRT: 421 AA.
AC 09VY89;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE YP3 PROTEIN.
GN YP3 OR CG11129.
OS Drosophila melanogaster (Fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Ephydroidea; Diptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Ephydroidea; Diptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OX NCCL_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chapple M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Planckoch C., Baldwin D.,
RA Bailey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandal D., Bolshakov S.,
RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Crawley S., Dahke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclio J.M.,
RA Palazolo M., Peltman G.S., Pan S., Pollard J.R., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Splitter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.-N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003493; AAF48314.1;
DR Flybase: FBgn0004047; YP3.
DR InterPro: IPR000901; Cpsase.
DR InterPro: IPR000734; Lipase.
DR Pfam: PF00151; Lipase; 1.
DR PROSITE: PS00867; Cpsase_2; UNKNOWN_1.
SQ SEQUENCE 421 AA; 46693 MW; 5BD4AAF75B0995DE CRC64;

Query Match 9.0%; Score 76.5; DB 5; Length 421;
Best Local Similarity 24.4%; Pred. No. 11;
Matches 39; Conservative 14; Mismatches 54; Indels 53; Gaps 7;

QY 8 MERIVICLMIYFLGLTVKSSSGQDR-----HMIRMLDID----- 45
DB 1 MMSLRICLLATCLLVAAHASKDASNDRLKPTKWLTALELVNSFLNDIWTWRLNQPLEQ 60
QY 46 -----VDOLKNYVNDLPFLPAPDEVENCSAFSCFOKAOLK-----SA 87
DB 61 GAKVTEKTIYHGQIK---HDLTSPFVSPSNVY---WIKSGQGVVECKLNNYVETAKA 114
QY 88 NTGNMERIINVSIRKL-KRPPSTNAGR-----OKHRL 120
DB 115 QPFGCEDEVITVLGDLPTSPAQOKAMRRLIOAYVOKYNL 154

Search completed: June 28, 2002, 07:44:35
Job time: 230 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:42:53 ; Search time 65.65 seconds

(without alignments)
237.113 Million cell updates/sec

Title: US-09-825-561a-10

Perfect score: 850
Sequence: 1 MRSSPGNMRIVICLVIFL.....LLQKMHQHSRTHGSEDS 162

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Indexed: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94.5	11.1	162	1 A53484	interleukin-15 pre
2	91.5	10.8	567	2 S29498	lymphocyte antigen
3	83	9.8	899	2 B38529	nibk protein - Esc
4	82	9.6	607	1 ABXL72	74k albumin precu
5	79	9.3	206	2 S49882	hypothetical prote
6	76.5	9.0	420	2 A25876	vitellogenin iii p
7	76.5	9.0	864	2 S60441	hypothetical prote
8	76	8.9	195	2 S60441	ureidoglycolate hy
9	75.5	8.9	336	2 S42632	Fit-15 protein pre
10	75.5	8.9	406	2 T28957	hypothetical prote
11	75.5	8.9	1206	2 S24407	formin isoform IV
12	75	8.8	321	2 T46352	hypothetical prote
13	74.5	8.8	286	2 F82881	hypothetical prote
14	74.5	8.8	482	2 S41211	voltage-dependent
15	74.5	8.8	789	2 S44759	cl1489.5 protein -
16	74	8.7	848	2 T00372	hypothetical prote
17	74	8.7	440	2 T47906	FUSCA PROTEIN FUS6
18	74	8.7	2	2 I48078	CHOL antigen - Chi
19	74	8.7	2197	2 B71600	variant-specific s
20	73.5	8.6	162	2 I49124	interleukin-15 - m
21	73.5	8.6	447	2 S39316	CAB30 protein - hu
22	73.5	8.6	472	2 I59087	ISG-R54 - human
23	73.5	8.6	477	2 S21049	calcium channel pr
24	73.5	8.6	484	2 A4608	voltage-dependent
25	73.5	8.6	484	2 S39315	CAB30 protein - hu
26	73.5	8.6	565	2 G89878	conserved hypotet
27	73.5	8.6	868	2 T31527	hypothetical prote
28	73.5	8.6	2118	2 T13612	hypothetical prote
29	73	8.6	234	2 G97966	hypothetical prote

30	73	8.6	304	2 A32108	translation initia
31	73	8.6	1291	2 T22382	hypothetical prote
32	72.5	8.5	309	2 T41889	PE38 orf153 - Bomb
33	72.5	8.5	380	2 T25454	hypothetical prote
34	72.5	8.5	667	2 D96923	uncharacterized co
35	72.5	8.5	1101	2 T26919	hypothetical prote
36	72	8.5	257	2 C69230	conserved hypotet
37	72	8.5	262	2 F72858	probable methyl tr
38	72	8.5	262	2 T41813	AcMNPV orf69 - Bom
39	72	8.5	546	2 G72210	hypothetical prote
40	72	8.5	719	2 T27977	lin-15a protein -
41	72	8.5	990	2 T43445	hypothetical prote
42	71.5	8.4	421	2 C84555	hypothetical prote
43	71.5	8.4	484	2 S62185	calcium channel be
44	71.5	8.4	674	2 S61181	hypothetical prote
45	71.5	8.4	741	2 A83317	isocitrate dehydro

ALIGNMENTS

RESULT 1
A53484
interleukin-15 precursor - green monkey
C:Species: Cercopithecus aethiops (green monkey, griwet)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A53484
R:Grabstein, K.H.; Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fung, V.;
; Girdl, J.G.
Science 264, 965-968, 1994
A:Title: Cloning of a T cell growth factor that interacts with the beta chain of the
A:Reference number: A53484; MUID:94233380
A:Accession: A53484
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-162 <GRA>
A:Cross-references: GB:U03099; NID:G493521; PIDN:AAA18416.1; PID:G493522
A:Note: the complete translation is not shown
C:Superfamily: interleukin-15
C:Keywords: growth factor
F:9-162/Product: interleukin-15 #status predicted <MAT>
F:93-133,90-136/Disulfide bonds: #status predicted

Query Match 11.1% Score 94.5; DB 1; Length 162;
Best Local Similarity 25.9%; Pred. No. 0.18; Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;
OY 43 IDIVDLKYNVDLVPF-----LPAPEDEVETNCWASFCF----OKAQLKSANTGNNE 93
DB 51 VNVISDLKK-IEDLIQSMHIDATLYESDVHPSCKYTKAKCFLEQVISHSGDTDHD 109
OY 94 RIINVSIRIKLRKPPSTNAGRRQKRLTCPSCDSYEKKPKPEFLERFKSLQKMH 149
DB 110 TVENLIIT--LANNILSSNGNITES---GCKECEELEKKIKELFSVAIVQMFIN 160
RESULT 2
S29498
Lymphocyte antigen Ly84 precursor - mouse
N:Alternate names: 38.5K T1 glycoprotein; ST2L protein
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 01-Dec-2000
C:Accession: S29498; A33541; S17657; S07054
R:Yanagisawa, K.; Takagi, T.; Tsukamoto, T.; Tetsuka, T.; Tomioka, S.
FEBS Lett. 318, 83-87, 1993
A:Title: Presence of a novel primary response gene ST2L, encoding a product highly si
A:Reference number: S29498; MUID:93170492
A:Accession: S29498
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-567 <YAN>
A:Cross-references: EMBL:D13695; NID:G286100; PIDN:BA02854.1; PID:G286101

R:Kleimenz, R., Hoffmann, S.; Weierstahl, A.K.
Proc. Natl. Acad. Sci. U.S.A. 86, 5708-5712, 1989
A:Title: Serum- and oncoprotein-mediated induction of a gene with sequence similarity to
A:Reference number: A33541; MUID:89345536
A:Accession: A33541
A:Molecule type: mRNA
A:Residues: 1-191, 'V', 193-328, 'SKECPSHIA' <KLE>
A:Cross-references: GB:M4843; NID:g201103; PIDN:AAA0160.1; PID:g201104
R:Tomlinaga, S.I.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Tetsuka, T.
Biochim. Biophys. Acta 1090, 1-8, 1991
A:Title: Molecular cloning of the murine ST2 gene. Characterization and chromosomal map
A:Reference number: S17657; MUID:91355215
A:Accession: S17657
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-191, 'V', 193-328, 'SKECPSHIA' <TOM>
A:Cross-references: EMBL:X60184; NID:954200; PIDN:CAA42742.1; PID:g54201
R:Tomlinaga, S.I.
FEBS Lett. 258, 301-304, 1989
A:Title: A putative protein of a growth specific cDNA from BALB/C-3T3 cells is highly si
A:Reference number: S07054; MUID:90092495
A:Accession: S07054
A:Molecule type: mRNA
A:Residues: 1-328, 'SKECPSHIA' <TO2>
A:Cross-references: EMBL:Y07519; NID:g5517; PIDN:CAA6812.1; PID:g5518
A:Note: It is uncertain whether Met-1, Met-7 or Met-19 is the initiator
C:Genetics:
A:Gene: ST2
A:Map position: 1
A:Introns: 27/1; 97/2; 155/3; 210/1; 233/1; 280/2
C:Superfamily: Interleukin-1 receptor type I
C:Keywords: glycoprotein
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-337/Product: ST2 protein #status predicted <MNT>
F:60,101,107,146,176,194,225,259,278/Binding site: carbohydrate (Asn) (covalent) #status

[illegible]

[illegible]

```

Query Match Similarity      9.0%; Score 76.5; DB 2; Length 420;
Best Local Similarity      22.4%; Pred. No. 22;
Matches      39; Conservative      14; Mismatches      54; Indels      53; Gaps      7;

OY      8 MERVIICIMVIFLGLTVHKSSQGD-----HMIRMOLIDI-----45
          | : ||| : : : | | |
DB       1 MMSLRICILACLVAAASHASKDASNDRLKPTKWLTATLEAVPSINDTWERLENPLEQ 60
          | : ||| : : : | | |

OY      46 -----VDLKKNVNDLYPEFLPAPEVENTCEWSASCFOKAOLK-----SA 87
          | : | : ||| : ||| : | : | : |
DB       61 GAKVEKIYHGQL-----HDLTPSFVPSPNVP---WIKSNGCKVECKLNVTETAKA 114
          | : | : ||| : ||| : | : | : |

OY      88 MTGNNERIINVSIIKKL-KRKPSTNAGRR-----QKHRL 120
          | : | : | : | : | : | : | : |
DB       115 QPGFGEDEVTLIVLTGLPKTSPAQOKAMRRLIQAYVQKYNL 154
          | : | : | : | : | : | : | : |

RESULT      7
S60441
hypothetical protein YGR150c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein G6642
C:Species: Saccharomyces cerevisiae
C:date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 29-Oct-1999
C:Accession: S60441; S64459
R:Skala, J.; Nawrocki, A.; Goffeau, A.
Yeast 11, 1421-1427, 1995
A:title: The sequence of a 27 kb segment on the right arm of chromosome VII from Sacc

A:Reference number: S60435; MUID:96158062
A:Accession: S60441
A:status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-864 <SKA>
A:Cross-references: EMBL:X85807; NID:g1045249; PIDN:CAA59608.1; PID:g1045256
R:Van Dyck, L.; Skala, J.; de Wergifosse, P.; Purnelle, B.; Tallia, E.; Nawrocki, A.;
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64428
A:Accession: S64459
A:Molecule type: DNA
A:Residues: 1-864 <VAN>
A:Cross-references: EMBL:Z72935; NID:g1323253; PIDN:CAA97164.1; PID:e243709; PID:g132
A:Experimental source: strain S288C
C:Genetics:
A:Map position: 7R

Query Match      9.0%; Score 76.5; DB 2; Length 864;
Best Local Similarity      22.5%; Pred. No. 48;
Matches      43; Conservative      22; Mismatches      59; Indels      67; Gaps      8;

OY      2 RSSPGNMERIYIC---LMVIFLGLTVHKSSQGDRHIMRMOLIDIVDLQKNYVNDLV 57
          | : | : | : | : | : | : | : | : |
DB       5 RCGPFKNM---VLCPFPQSLFLEFSKRLINK-----RFKYTLQTEDE-KMMGSLS 49
          | : | : | : | : | : | : | : | : |

OY      58 PEPLPADPDVENECWSAFSCFOKAOLKSANTGNNERIINVSIIKKLRKPSTNAGRROK 117
          | : | : | : | : | : | : | : | : |
DB       50 KKKITPPDVE-----FKLAQLREBSNTLTKERHNKK-----SVNSDGHS 90
          | : | : | : | : | : | : | : | : |

OY      118 HRLTCPCSDSYEKRPK-----EFLERFKSLQKMIHQ-----150
          | : | : | : | : | : | : | : | : |
DB       91 NSIAPISEDSRNVNVTAKSSVPNEEKSKNLSDLIHSSFLEKMMDLLVPRKVIREFRAADDIL 150
          | : | : | : | : | : | : | : | : |

OY      151 --HLSRTGCS 159
          | : | : | : | : | : | : | : | : |
DB       151 AKNLFDRSHSN 161
          | : | : | : | : | : | : | : | : |

RESULT      8
S42022
ureidoglycolate hydrolase (EC 3.5.3.19) - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YIR032c

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Db 377 ITAGTSGHSTST-----DYNKELAEKMEV--FKPTHPOLLOTKA----- 414
QY 77 SCFOKAOLKSANTGNNERIIV-----SIKKLK-RKPSTNAGRQKHRLTCPSCD 126
Db 415 SAMNSNAVSPANTNSDEIECVYOGPPKTPASIKRIQTEGPRTLGQRMKSTLSVPAHQ 474
QY 127 SYEKRPKEFLERFKSLQKMIHQ 150
Db 475 RSSIIPVYKTEDEAMECLSMME 498

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Search completed: June 28, 2002, 07:42:56
 Job time: 131 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 28, 2002, 07:43:20 ; Search time 20.33 Seconds
(without alignments)
308.537 Million cell updates/sec

Title: us-09-825-561a-10

Sequence: 1 MRSSPGMNERIVICLAWIFL.....LLOKTIHQHLSRTHGSEDS 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 105224 seqs, 36719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106.5	12.5	162	IL15_FELCA	O97687 felis silve
2	99.5	11.7	162	IL15_HUMAN	P40933 homo sapien
3	94.5	11.1	162	IL15_CERAE	P40221 cercopithec
4	94.5	11.1	162	IL15_MACMU	P48092 macaca mula
5	91.5	10.8	337	IRL1_MOUSE	P14719 mus musculu
6	90.5	10.6	162	IL15_BOVIN	Q28028 bos taurus
7	90.5	10.6	162	IL15_SHEEP	O94316 ovvis aries
8	82	9.6	607	ALB2_XENLA	P14872 xenopus lae
9	80.5	9.5	162	IL15_PIG	O95253 sus scrofa
10	79	9.3	206	YIM7_YEAST	P40470 saccharomyc
11	78	9.2	741	IDH_AZOVI	P16100 azotobacter
12	77	9.1	856	KNS5_HUMAN	Q02241 homo sapien
13	76.5	9.0	420	VIR3_DROME	P06607 drosophila
14	76.5	9.0	864	Y63M_YEAST	P48237 saccharomyc
15	76	8.9	195	ALIA_YEAST	P32459 saccharomyc
16	75.5	8.9	133	IL4_FELCA	P55030 felis silve
17	75.5	8.9	1206	FM14_MOUSE	O05859 mus musculu
18	75	8.8	334	LCMT_HUMAN	Q9uic8 homo sapien
19	74.5	8.8	441	FUS6_ARATH	P45432 arabidopsi
20	74.5	8.8	789	YK25_CAEEL	P34332 caenorhabdi
21	73.5	8.6	162	IL15_MOUSE	P48346 mus musculu
22	73.5	8.6	472	IFM2_HUMAN	P09919 homo sapien
23	73.5	8.6	477	CCR3_PABIT	P54286 onychotylus
24	73.5	8.6	484	CCR3_HUMAN	P54284 homo sapien
25	73.5	8.6	484	CCR3_RAT	P54287 rattus norv
26	73	8.6	304	IF2A_YEAST	P20459 saccharomyc
27	72.5	8.5	162	IL15_RAT	P97604 rattus norv
28	72	8.5	262	Y069_NPVAC	P41469 autographa
29	71.5	8.4	484	CCR3_MOUSE	P54285 mus musculu
30	71.5	8.4	2758	IP3R_HUMAN	O14643 homo sapien
31	71	8.4	805	AHR_MOUSE	P30561 mus musculu
32	70	8.2	403	IF73_MOUSE	O64345 mus musculu
33	70	8.2	739	BAC1_MOUSE	P97302 mus musculu

34	70	8.2	1222	1	YMP3_CAEEL	Q10947 caenorhabdi
35	70	8.2	1230	1	SMC3_YEAST	P47037 saccharomyc
36	70	8.2	1636	1	BUD3_YEAST	P25558 saccharomyc
37	69.5	8.2	219	1	Y413_RICPR	O92509 rickettsia
38	69.5	8.2	678	1	Y564_TREPA	O83575 treponema p
39	69.5	8.2	1468	1	FMN1_MOUSE	O05860 mus musculu
40	69.5	8.2	1750	1	Y832_METUA	O58242 methanococc
41	69	8.1	132	1	IL4_CANFA	O77762 canis famli
42	69	8.1	568	1	FTS1_BUCAP	O85297 buchnera ap
43	69	8.1	932	1	PMS1_HUMAN	P54277 homo sapien
44	68.5	8.1	464	1	N2B_HAEIR	P46441 haematobia
45	68.5	8.1	655	1	YDH2_SCHPO	O92347 schizosacch

ALIGNMENTS

RESULT	ID	IL15_FELCA	STANDARD:	PRT:	162 AA.
AC	O97687				
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	30-MAY-2000 (Rel. 39, Last annotation update)				
DE	Interleukin-15 precursor (IL-15).				
GN	IL15.				
OS	Felis silvestris catus (Cat).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.				
OX	NCBI_Taxid=9685;				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Lymph node;				
RA	Barger A.B., Dean G.A., Layoy A.S.;				
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.				
CC	-1- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-				
CC	LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15				
CC	WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R				
CC	GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: Secreted.				
CC	-1- SIMILARITY: BELONGS TO THE IL-15 FAMILY.				
CC	-----				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
CC	EMBL; AF108148; AAD05268.1; -				
DR	InterPro: IPR003443; Interleukin_15.				
DR	Pfam: PF02372; IL15; 1.				
FW	Cyclokin; Glycoprotein; Signal.				
FT	SIGNAL 1 29				
FT	PROPEP 30 48				
FT	POTENTIAL.				
FT	CHARN 49 162				
FT	DISULFID 83 133				
FT	DISULFID 90 136				
FT	CARBOHYD 104 104				
FT	CARBOHYD 127 127				
FT	SEQUENCE 162 AA; 18412 MW; D8C7CEFFA0110DD CRC64;				
QY	14 CLAWFLGTLT---VHKSSGOGDRHMTFRMQLDIYDQKYNVNDLVPEFLPAPDEVETN 70				
DB	30 CIPVFILSCINAGLPKTEANMOD--VTSDKIITDKIISLHIDATLYTE-----SVYHN 82				
QY	71 CEWSAFSCF---OKAOLKSNANGNNERNITNVSIKIKLRKRPSTNAGRRQKRLT---CP 123				

Query Match 12.5% Score 106.5; DB 1; Length 162;
Best Local Similarity 26.0%; Pred. No. 0.0042;
Matches 38; Conservative 25; Mismatches 58; Indels 25; Gaps 6;

Db 83 CRYTAMCFLLEHLVLSLEKNEIHOQTVENII-----LANGSLSNRITETGCK 134
QY 124 SCDSYEKKPKREFLEPKSLÖKMÖH 149
Db 135 ECELEEKNIKEFLQSFVHIQMFEN 160

RESULT 2
IL15_HUMAN STANDARD; PRT; 162 AA.
ID IL15_HUMAN
AC P40933; Q93058; O43512; O00440; Q9QBAD;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-15 precursor (IL-15).
GN IL15.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_Taxid=9606;
[1]
SEQUENCE FROM N.A. (IL15-S48AA ISOFORM).
RC TISSUE=bone marrow;
RX MEDLINE=94233380; PubMed=8178155;
RA Grabschtein K.K., Eisenman J., Sheanbeck K., Rauch C.,
RA Srinivasan S., Fung V., Beers C., Richardson J., Schoenborn M.A.,
RA Anhieh M., Johnson L., Alderson M.R., Watson J.D., Anderson D.M.,
RA Gali J.G.;
RT "Cloning of a T cell growth factor that interacts with the beta chain
RT of the interleukin-2 receptor.";
RT Science 264:965-968(1994).
RN [2]
RP SEQUENCE FROM N.A. (IL15-S48AA ISOFORM).
RA Kiese H., Jandrig B., Wernicke C., Bulfone-Paus S., Pohl T.,
RA Diamantstein T.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (IL15-S21AA ISOFORM).
RC TISSUE=Lung cancer;
RX MEDLINE=96218668; PubMed=866345;
RA Meazza R., Verdiani S., Blassoni R., Coppolecchia M., Gaggero A.,
RA Orenzo A.M., Colombo M.P., Azzone B., Ferrini S.;
RT "Identification of a novel interleukin-15 (IL-15) transcript isoform
RT generated by alternative splicing in human small cell lung cancer
RT cell lines.";
RL Oncogene 12:2187-2192(1996).
RN [4]
RP SEQUENCE FROM N.A. (IL15-S21AA ISOFORM).
RC TISSUE=Testis;
RX MEDLINE=98070771; PubMed=9405632;
RA Tagaya Y., Kurys G., Thies T.A., Losi J.M., Azimi N., Hanover J.A.,
RA Banford R.N., Waldman T.A.;
RT "Generation of secretable and nonsecretable interleukin 15 isoforms
RT through alternate usage of signal peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:1444-1449(1997).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RA Meazza R., Ferrini S.;
RT "Expression of two IL-15 mRNA isoforms in human tumors does not
RT correlate with secretion: role of different signal peptides.";
RL submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 49-162 FROM N.A.
RC TISSUE=Epidermis;
RA Sorel M.A., Jacques Y.;
RT "IL15 expression in human keratinocytes.";
RL submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
CC LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
CC WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
CC GAMMA BUT NOT IL-2R ALPHA.
CC -1- SUBCELLULAR LOCATION: SECRETED (IL15-S48AA). IL15-S21AA IS NOT

[illegible]

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RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 49-81.
RC TISSUE=Kidney;
RX MEDLINE=94233380; PubMed=8178155;
RA Strabstein K.H., Eisenman J., Shanebeck K., Rauch C.,
RA Strabstein S., Fung V., Beers C., Richardson J., Schoenborn M.A.,
RA Adie M., Johnson L., Alderson M.R., Watson J.D., Anderson D.M.,
RA Gilt J.G.;
RT "Cloning of a T cell growth factor that interacts with the beta chain
RT of the Interleukin-2 receptor.";
RL Science 264:965-968(1994).
CC -1- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
CC LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
CC WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
CC GAMMA BUT NOT IL-2R ALPHA.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U03099; AAA18416.1; -
DR InterPro: IPR003443; Interleukin_15.
DR Pfam: PF02372; IL15; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 29 POTENTIAL.
FT PROPEP 30 48
FT CHAIN 49 162 INTERLEUKIN-15.
FT DISULFID 83 133 POTENTIAL.
FT DISULFID 90 136
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 162 AA; 18222 MW; 1BF9A82644E1C9B7 CRC64;

Query Match 11.1%; Score 94.5; DB 1; Length 162;
Best Local Similarity 25.9%; Pred. No. 0.054;
Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;

QY 43 IDIVDLKNTVNDLVEF-----LPAPDEVETNCESASFCF-----QKOLKSANTGNNE 93
DB 51 VNVISDLKK-IEDLDSMHIDATLYTESDVHPSCKYAKMCFLELQVISHESGDTIHD 109
94 RIINVSIKLKRRPSTNAGRQKHRLTCPSCSYEKRPKEFLERFKSLQKMH 149
110 TVENLIIT--LANNILISNGNITES---GCKECBELERKNIKEFLQSFVHIYOMFIN 160

RESULT 4
IL15_MACMU STANDARD; PRT; 162 AA.
AC P48092;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-15 precursor (IL-15).
GN IL15.
OS Macaca mulatta (Rhesus macaque).
OC Mammalia; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Cercopitheciinae; Primates; Catarrhini; Cercopitheciidae;
OC NCBL_TaxID=9544;
OX NCBL_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Vulliamer F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";

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RL J. Immunol. 155:3946-3954(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Tatsumi M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
CC LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
CC WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
CC GAMMA BUT NOT IL-2R ALPHA.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U19843; AAB60398.1; -
DR EMBL: AB000555; BAA19149.1; -
DR InterPro: IPR003443; Interleukin_15.
DR Pfam: PF02372; IL15; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 29 POTENTIAL.
FT PROPEP 30 48
FT CHAIN 49 162 INTERLEUKIN-15.
FT DISULFID 83 133 POTENTIAL.
FT DISULFID 90 136
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 5 5 K -> T.
FT VARIANT 31 31 I -> T.
SQ SEQUENCE 162 AA; 18194 MW; D233CF7FF6188C01 CRC64;

Query Match 11.1%; Score 94.5; DB 1; Length 162;
Best Local Similarity 25.9%; Pred. No. 0.054;
Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;

QY 43 IDIVDLKNTVNDLVEF-----LPAPDEVETNCESASFCF-----QKOLKSANTGNNE 93
DB 51 VNVISDLKK-IEDLDSMHIDATLYTESDVHPSCKYAKMCFLELQVISHESGDTIHD 109
94 RIINVSIKLKRRPSTNAGRQKHRLTCPSCSYEKRPKEFLERFKSLQKMH 149
110 TVENLIIT--LANNILISNGNITES---GCKECBELERKNIKEFLQSFVHIYOMFIN 160

RESULT 5
IRL_MOUSE STANDARD; PRT; 337 AA.
ID IRL_MOUSE
AC P14719;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin 1 receptor-like 1 precursor (ST2 protein) (T1 protein)
DE (Lymphocyte antigen 84).
GN ILIRL1 OR ST2 OR STP2 OR LY84.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBL_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=90092495; PubMed=2532153;
RA Tomimaga S.;
RT "A putative protein of a growth specific cDNA from BALB/C-3T3 cells
RT is highly similar to the extracellular portion of mouse interleukin 1
RT receptor.";
RL FEBS Lett. 258:301-304(1989).
RN [2]

```

Query Match	Best Local Similarity	Score	DB 1:	Length	337:
Matches 33; Conservative	25.68%	Pred. NO. 0.23;	Mismatches 39; Indels	37;	Gaps 7;
47 DOLKRYVNDLVEFELPAEDVETNCEWMSAFSCFOAKOLKSANTGNNERTIINVSIIKKLRK	100	100	100	100	100
76 DRK-----FLPAVE-----DSGLTAYC-----IRSPUL-NKTGYLVNTIHK-----K	113	113	113	113	113
107 PPSTN-----AGRRQKHRLTCPCSDSYEKRRPKPEFLERFSLLQKMHQ-----	151	151	151	151	151
114 PPSCHIPDYLMYSTVRGSDKNFKIKTCPTIDLYNMTAPVQWFKNCALQDPRFAHRYLF	173	173	173	173	173

[illegible]

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ID IL15_SHEEP STANDARD; PRT; 162 AA.
AC OX9XSJ6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Interleukin-15 precursor (IL-15).
GN IL15.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_Taxid=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Casey G.J., Chaplin P.J.;
RT "Isolation of interleukin-15 mRNA transcripts from T and B cells
RT circulating in effluent lymph."
RL J. Interferon Cytokine Res. 0:0-0(1999).
CC -1- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
CC LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
CC WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
CC GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
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CC -----
DR EMBL: AF149700; AAD37425.1; -.
DR InterPro: IPR003443; Interleukin_15.
DR Pfam: PF02372; IL15.1.
DR CYTOKINE; Glycoprotein; Signal.
KM SIGNAL 1 29
FT PROPEP 30 48 POTENTIAL.
FT CHAIN 49 162 POTENTIAL.
FT DISULFID 83 133 INTERLEUKIN-15.
FT DISULFID 90 136 POTENTIAL.
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 162 AA; 18510 MW; 87195650E45F1E5D CRC64;

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Query Match 10.6%; Score 90.5; DB 1; Length 162;
Best Local Similarity 22.0%; Pred. No. 0.13; Mismatches 4;
Matches 33; Conservative 24; Indels 19; Gaps 4;

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OS Xenopus laevis (African Clawed Frog).
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_Taxid=6355;
RN [1]
RP SEQUENCE OF 3-607 FROM N.A.
RX MEDLINE=89313788; PubMed=2747653;
RA Moskaitis J.E., Sargent T.D., Smith L.H. Jr., Pastori R.L.,
RA Schoenberg D.R.;
RT "Xenopus laevis serum albumin: sequence of the complementary
RT deoxyribonucleic acids encoding the 68- and 74-kilodalton peptides
RT and the regulation of albumin gene expression by thyroid hormone
RT during development."
RL Mol. Endocrinol. 3:464-473(1989).
RN [2]
RP SEQUENCE OF 1-48 FROM N.A.
RX MEDLINE=88172470; PubMed=2451026;
RA Schorpp M., Doeberling U., Wagner U., Ryffel G.U.;
RT "5'-flanking and 5'-proximal exon regions of the two Xenopus albumin
RT genes. Deletion analysis of constitutive promoter function."
RL J. Mol. Biol. 199:83-93(1988).
RN [3]
RP SEQUENCE OF 459-557 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=85126974; PubMed=3971963;
RA Wolffe A.P., Glover J.F., Martin S.C., Tenniswood M.P.R.,
RA Williams J.L., Tata J.R.;
RT "Deletion of transcription of Xenopus 74-kDa albumin genes and
RT destabilization of mRNA by estrogen in vivo and in hepatocyte
RL cultures."
RL Eur. J. Biochem. 146:489-496(1985).
CC -1- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
CC BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
CC -----
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CC -----
DR EMBL: M21442; AAA49637.1; -.
DR EMBL: M28276; AAA49642.1; -.
DR PIR: B41682; ABXL72.
DR HSSP: P02768; IBJ5.
DR InterPro: IPR000264; Serum_albumin.
DR Pfam: PF00273; transport_prot. 3.
DR PRINTS: PR00802; SERUMALBUMIN.
DR ProDom: PD002486; Serum_albumin. 1.
DR SMART: SM00103; ALBUMIN; 3.
DR PROSITE: PS00212; ALBUMIN; 3.
KW Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
KW Copper.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 24 POTENTIAL.
FT CHAIN 25 607 74 KDA SERUM ALBUMIN.
FT REPEAT 29 211 1.
FT REPEAT 217 403 2.
FT REPEAT 409 601 3.
FT METAL 30 30 COPPER (BY SIMILARITY).
FT DISULFID 80 88 BY SIMILARITY.
FT DISULFID 101 117 BY SIMILARITY.
FT DISULFID 116 127 BY SIMILARITY.
FT DISULFID 147 192 BY SIMILARITY.
FT DISULFID 191 200 BY SIMILARITY.

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RESULT 11
IDH_AZOVI STANDARD: PRT: 741 AA.
AC IDH_AZOVI
PI6100:
DT 01-APR-1990 (Rel. 14, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Isocitrate dehydrogenase [NADP] (EC 1.1.1.42) (Oxalosuccinate
decarboxylase) (IDH).
GN ICD.
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RA Sahara T., Suzuki M., Tsuruha J.I., Takada Y., Abe K., Fukunaga N.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
[2]
PRELIMINARY SEQUENCE OF 228-250 AND 254-259.
RA Edwards D.J., Heinrichson R.L., Chung A.E.;
MEDLINE=74086945; PubMed=4149369;
RT "Triphosphopyridine nucleotide specific isocitrate dehydrogenase from
Azotobacter vinelandii. Alkylation of a specific methionine residue
and amino acid sequence of the peptide containing this residue.";
RL Biochemistry 13:677-683(1974).
CC -1 CATALYTIC ACTIVITY: Isocitrate + NADP(+) = 2-oxoglutarate + CO(2)
+ NADPH.
CC -1 ENZYME REGULATION: INHIBITION OF THIS ENZYME BY PHOSPHORYLATION
REGULATES THE BRANCH POINT BETWEEN THE KREBS CYCLE AND THE
GLYOXALATE BYPASS, WHICH IS AN ALTERNATE ROUTE THAT ACCUMULATES
CARBON FOR BIOSYNTHESIS WHEN ACETATE IS THE SOLE CARBON SOURCE
FOR GROWTH. THE PHOSPHORYLATION STATE OF THIS ENZYME IS CONTROLLED
BY ISOCITRATE DEHYDROGENASE KINASE/PHOSPHATASE (ACEK).
CC -1 SUBUNIT: MONOMER.
CC -1 SIMILARITY: BELONGS TO THE MONOMERIC-TYPE FAMILY OF IDH.
-----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D73443; BA011169.1; -
DR PIR: A10759; A10759.
CC Oxidoreductase; NADP: Phosphorylation; Glyoxylate bypass;
CC Tricarboxylic acid cycle.
CC SEQUENCE 741 AA; 80389 MW; 29FE35278E5AED8B CRC64;
SQ

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GN KNSL5 OR MKLPI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93024924; PubMed=1406973;
RA Nislow C., Lombillo V.A., Kuriyama R., McIntosh J.R.;
RT "A plus-end-directed motor enzyme that moves antiparallel
microtubules in vitro localizes to the interzone of mitotic
spindles.";
RL Nature 359:543-547(1992).
RN [2]
RP REVISIONS.
RA Gryka M.A.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1 FUNCTION: PLUS-END-DIRECTED MOTOR ENZYME THAT MOVES ANTIPARALLEL
CC MICROTUBULES IN VITRO. LOCALIZES TO THE INTERZONE OF MITOTIC
CC SPINDLES.
CC -1 SUBCELLULAR LOCATION: Nuclear.
CC -1 SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
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CC -----
DR EMBL: X67155; CAA47628.2; -
DR PIR: S28262; S28262.
DR HSSP: P33176; 1B32.
DR MIM: 605064; -
DR InterPro: IPR001752; kinesin.
DR Pfam: PF00225; kinesin; 1.
DR PRINTS: PR00380; KINESINHEAVY.
DR SMART: SM00129; KISC; 1.
DR PROSITE: PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE: PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KW Motor protein; Cell division; Microtubules; ATP-binding; Coiled coil;
KW Mitosis; Cell cycle; Nuclear protein.
FT DOMAIN 1 352 KINESIN-MOTOR.
FT DOMAIN 535 620 COILED COIL (POTENTIAL).
FT DOMAIN 7 11 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT NP_BIND 112 119 ATP (BY SIMILARITY).
SQ SEQUENCE 856 AA; 98105 MW; DDE7CEB480ABE58A CRC64;

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Query Match 9.2%; Score 78; DB 1; Length 741;
Best Local Similarity 24.8%; Pred. No. 10;
Matches 26; Conservative 23; Mismatches 34; Indels 22; Gaps 4;
OY 33 DRHMTRMQLIDVDOLKNVNDL-----VPEFLPAEDVETNCESAFSCFOKAOLKS 86
I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I:::
DB 77 DANIKLKNISASVQALKAELKELQOOGYKLPDY---PEBKTDPEKDVKARYDKIGSA 133
OY 87 AN-----TGNNRIINVSIKKLKRPSPNAGRRKQKRLTSCSCS 127
I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I:::
DB 134 VNPVLRSGNSDRAPLQVKNYARKHP-----HKMGWSADS 169

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Query Match 9.1%; Score 77; DB 1; Length 856;
Best Local Similarity 22.9%; Pred. No. 15;
Matches 44; Conservative 32; Mismatches 70; Indels 46; Gaps 10;
OY 1 MRSSPGMERIVICLVNPF--IGTL-----YKSSQGGDRMIMRQLIDVDOLKNIV 53
I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I:::
DB 122 MTGSPGEGGLPRCLDMITNIGSFQAKRYKFSN---DRSMNIDCEVDAL--LEKOK 175
OY 54 NDLVP-----EFLPAEDVETNCESAFSCFOKAOLKSANTGN 91
I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I:::
DB 176 REMAMPKTSRSSKQYDPEPADMITVOEFCKA--EEVDESVYGVVSY---IETLYNNIT 230
I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I:::
OY 92 NERIINVSIKKLKRPSPNAGRRKQKRLTSCSCS-----KSLDQKMI 148
I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I:::
DB 231 YDLLEVPDPKPKPQSKLLREDKNHMYVACGEVEVSKTEAEAFVFMGQKKRRRIA 290
I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I:::
OY 149 HQHL-----SKRTH 157
I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I::: I:::
DB 291 NTRALNRESSRSH 302

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RESULT 13
VIT3_DROME

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ID VIT3_DROME STANDARD: PRT; 420 AA.
AC P06607;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vitellogenin III precursor (Yolk protein 3).
GN YP3.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S;
RX MEDLINE=87305580; PubMed=31114046;
RA Garabedian M.J., Shiras A.D., Bownes M., Wensink P.C.;
RT "The nucleotide sequence of the gene coding for Drosophila
RL melanogaster yolk protein 3.";
RL Gene 55:1-8(1987).
[2]
SEQUENCE FROM N.A.
MEDLINE=87146365; PubMed=3029679;
RA Yan Y.L., Kunert C.J., Postlethwait J.H.;
RT "Sequence homologies among the three yolk polypeptide (Yp) genes in
RL Drosophila melanogaster.";
RN Nucleic Acids Res. 15:67-85(1987).
[3]
SEQUENCE FROM N.A. (MUTANT YP3S1).
RX MEDLINE=91360094; PubMed=1909425;
RA Liddell S., Bownes M.;
RT "Characterization, molecular cloning and sequencing of YP3s1, a
RL fertile yolk protein 3 mutant in Drosophila.";
RL Mol. Gen. Genet. 228:81-88(1991).
CC -1- FUNCTION: VITELLOGENIN IS THE MAJOR YOLK PROTEIN OF EGGS WHERE
CC IT IS USED AS A FOOD SOURCE DURING EMBRYOGENESIS.
CC -1- TISSUE SPECIFICITY: SYNTHESIZED IN THE FAT BODY AND OVARIAN
CC FOLLICLE CELLS AND ACCUMULATE IN THE OOCYTE.
CC -1- INDUCTION: By beta-ecdysone; in males.
CC -1- MISCELLANEOUS: THE MUTANT YP3-S1 IS SYNTHESIZED IN THE FAT BODY,
CC BUT NOT SECRETED, PROBABLY DUE TO THE AMINO ACID MUTATION IN THE
CC SIGNAL PEPTIDE.
CC -1- SIMILARITY: PARTIAL, TO LIPASES. STRONG TO OTHER VITELLOGENINS.
CC
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CC or send an email to license@isb-sib.ch).
DR EMBL: M15898; AAA29024.1; -
DR EMBL: X04754; CAA28451.1; -
DR PIR: A27388; A27388.
DR PIR: A25876; A25876.
DR FLYBASE: FBgn0004047; YP3.
DR InterPro: IPR000734; Lipase.
DR Pfam: PF00151; Lipase; 1.
KW Yolk; Signal.
FT SIGNAL 1 19
FT CHAIN 20 420 VITELLOGENIN III.
FT VARIANT 10 10 A -> D (IN MUTANT YP3S1).
SQ SEQUENCE 420 AA; 46101 MW; 5457C49CAC933B26 CRC64;

Query Match 9.0%; Score 76.5; DB 1; Length 420;
Best Local Similarity 24.4%; Pred. No. 7.4;
Matches 39; Conservative 14; Mismatches 54; Indels 53; Gaps 7;
OY 8 MERIVICLVWIFGLVHSSSGODR-----HMIRKRLIDI----- 45
DB 1 MMSLRICLATCLVAHAHSAKSDANDRLKPTKWTATLETENVPSLNDITWERTLENPLEQ 60

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OY 46 -----VDOLKNVNDLVEPLPAPEDVETNCWSAFSCFOKAOLK-----SA 87
DB 61 GAKYIEIYVGOIK---HDLTPSEVPSPSNVY---WIKSGQAVECKINNYVETAA 114
OY 88 NTGNNERIINVSIRKL-KRKPSTNAGR-----QKHRL 120
DB 115 QPGGEDEVITVLGLPKTSPAQOKAMRRLIQAVQKYNL 154

RESULT 14
ID YG3M_YEAST STANDARD: PRT; 864 AA.
AC P48237;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 101.4 kDa protein in RPL4B-NSRI intergenic region.
GN YGR150C OR G6642.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C;
RX MEDLINE=96158062; PubMed=8585325;
RA Skala J., Nawrocki A., Goffeau A.;
RT "The sequence of a 27 kb segment on the right arm of chromosome VII
RL from Saccharomyces cerevisiae reveals MOLI, NAT2, RPL30B, RSRI, CY54,
RL PEX1/CHO2, NSRI genes and ten new open reading frames.";
RL Yeast 11:1421-1427(1995).
CC -1- SIMILARITY: SOME, TO S.POMBE SPBC1967.07C.
CC
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DR EMBL: X85807; CAA59808.1; -
DR EMBL: Z72935; CAA97164.1; -
DR SGD: S0003382; YGR150C.
DR InterPro: IPR002885; PPR.
DR Pfam: PF01535; PPR; 1.
KW Hypothetical protein.
SQ SEQUENCE 864 AA; 101422 MW; 5A773DEAA33D84FE CRC64;

Query Match 9.0%; Score 76.5; DB 1; Length 864;
Best Local Similarity 22.5%; Pred. No. 17;
Matches 43; Conservative 22; Mismatches 59; Indels 67; Gaps 8;
OY 2 RSSPGNMRIVIC---LMVIFELGTVHKSSSQGDHMI RMRLDIYDOLKNVNDLV 57
DB 5 RCGPRKN---VLCEPFOISLFESKRLINK-----RFKTTDTEDE-KMMGSLS 49
OY 58 PEFLPAPEDVETNCWSAFSCFOKAOLKSANTGNNERIINVSIRKLKRKPSTNAGROR 117
DB 50 KNKITTPEDEV-----FKLAQLRFPSTNLKEIHNTK-----SYNSDGHQS 90
OY 118 HRLTCPCSDSYEKRPK-----EFLERFSLQAKMTHQ----- 150
DB 91 NSIAPISDSRNNAVVTSSVPENEKSKNLSDLIHSFLEKMDHLYPKVIRRYADDDIL 150
OY 151 --HLSRTHGS 159
DB 151 AKNLFDRSHSN 161

RESULT 15

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ALLA_YEAST
ID ALLA_YEAST STANDARD: PRT; 195 AA.
AC P32459;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ureidoglycolate hydrolase (EC 3.5.3.19).
GN DAL3 OR YIR032C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92133160; PubMed=1776360;
RA Yoo H.S., Cooper T.G.;
RT "The ureidoglycolate hydrolase (DAL3) gene in Saccharomyces
ceriseiae";
RT Yeast 7:693-698(1991).
[2]
NP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
RA Churcher C.M., Connor R., Copsey R., Dear S., Devlin K., Fraser A.,
RA Gentles S., Hamlyn N., Hornell T.S., Hunt S., Jagels K., Jones M.,
RA Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
RA Rajandream M.A., Riles L., Rowley N., Skellon J., Smith V.,
RA Walsh S.V., Whitehead S.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: UTILIZATION OF PURINES AS SECONDARY NITROGEN SOURCES,
CC WHEN PRIMARY SOURCES ARE LIMITING.
CC -! CATALYTIC ACTIVITY: (-)-ureidoglycolate + H(2)O = glyoxylate + 2
CC NH(3) + CO(2).
CC -! PATHWAY: THIRD STEP IN THE DEGRADATION OF ATLANTOIN (PURINE
CC CATABOLISM).
CC -----
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CC -----
DR EMBL; M64778; AAA73025.1; -.
DR EMBL; Z38061; CAA86192.1; -.
DR PIR; S42022; S42022.
DR PIR; S48494; S48494.
DR SDD; S0001471; DAL3.
KM Hydrolyase; Purine metabolism; Prenylation; Lipoprotein.
FT LIPID 192 FARNESYL (BY SIMILARITY).
SQ SEQUENCE 195 AA; 21727 MW; 6230AEB69585206B CRC64;

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Query Match 8.9%; Score 76; DB 1; Length 195;
 Best Local Similarity 27.6%; Pred. No. 3.4; Mismatches 29; Indels 20; Gaps 3;
 Matches 24; Conservative 14;

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OY 24 VHKSSGQGRHMRKLDIVDOLKNTVNDVPEFLPAPEDVETNCWSAFSCFOKQ 83
   :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 33 LEKGANGT---AIKLLQ---VSQVENKSTKVP-----NMNLFRCFPDPH 72
   :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 84 LKSANTGNERRIINVSIIKIKRRKPPST 110
   :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 73 LNRVFTGSGNQAIASHISIKVLEKHPGST 99
   :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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Search completed: June 28, 2002, 07:43:22
 Job time: 157 sec

